

36/985

Title: Modulating developmental pathways in plants.

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The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

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Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5    Y14600|SBRLK1|*Sorghum bicolor*  
BF004020|BF004020|EST432518 *KV1 Medicago truncatata*  
AW934655|AW934655|EST353547 *tomato*  
AW617954|AW617954|EST314028 *L. pennellii*  
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
- 10   AA738545|AA738545|SbRLK3 *Sorghum bicolor*  
BG595415|BG595415|EST494093 *cSTS Solanum tuberosa*  
AI896277|AI896277|EST265720 *tomato*  
BF643238|BF643238|NF002H05EC1F1045  
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
- 15   BE658174|BE658174|GM700005A20D5 *Gm-r1070 Glycine max*  
BF520845|BF520845|EST458318 *DSIL Medicago truncata*  
AC069324|AC069324|*Oryza sativa*  
AW761055|AW761055|sl70d06.y1 *Gm-cl027 Glycine max*  
BE352622|BE352622|WHE0425\_G11\_M21ZS *Wheat*
- 20   BG647340|BG647340|EST508959 *HOGA Medicago truncata*  
AY028699|AY028699|*Brassica napus*  
AW666082|AW666082|sk31h04.y1 *Gm-cl028 Glycine max*  
AA738547|AA738547|SbRLK5 *Sorghum bicolor*  
BG127658|BG127658|EST473220 *tomato*
- 25   L27821|RICPRKI|*Oryza sativa*  
BG238468|BG238468|sab51a09.y1 *Gm-cl043 Glycine max*  
BG441204|BG441204|GA\_Ea0012C15f *Gossypium arbo.*  
AW667985|AW667985|GA\_Ea0012C15 *Gossypium arbore.*  
AW233982|AW233982|sf32g05.y1 *Gm-cl028 Glycine max*
- 30   AF003235|AF003235|*Oryza sativa*  
BF460294|BF460294|074A05 *Mature tuber*  
AY007545|AY007545|*Brassica napus*  
AC087544|AC087544|*Oryza sativa*  
AB041503|AB041503|*Populus nigra*
- 35

The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.  
 However, they lack a transmembrane domain while they do  
 contain a signaling sequence at the N-terminal end. Therefore  
 these proteins are thought to be positioned within vesicles  
 5 within the plant cell or at the outside of the plasma  
 membrane, within the cell wall of the plant cell. A number of  
 homologs have been detected in other plant species, such as:

- AF370543|AF370543|*Arabidopsis thaliana*  
 10 AF324989|AF324989|*Arabidopsis thaliana*  
AV520367|AV520367|*Arabidopsis thaliana*  
AV553051|AV553051|*Arabidopsis thaliana*  
BF642233|BF642233|NF050C09IN1F1069  
AW559436|AW559436|EST314484 *DSIR Medicago truncata*  
 15 BG456991|BG456991|NF099F02PL1F1025  
AW622146|AW622146|EST312944 *tomato*  
BF260895|BF260895|HVSMEF0023D15f *Hordeum vulgare*  
BE322325|BE322325|NF022E12IN1F1088  
BG414774|BG414774|HVSMEK0003K21f *Hordeum vulgare*  
 20 BE460627|BE460627|EST412046 *tomato*  
BI204894|BI204894|EST522934 *CTOS Lycopersicon esculentum*  
BI205306|BI205306|EST523346 *CTOS Lycopersicon esculentum*  
BI204366|BI204366|EST522406 *CTOS Lycopersicon esculentum*  
AW443205|AW443205|EST308135 *tomato*  
 25 AW031110|AW031110|EST274417 *tomato*  
BI180080|BI180080|EST521025 *cSTE Solanum tuberosa*  
BF644761|BF644761|NF015A11EC1F1084  
AV526127|AV526127|*Arabidopsis thaliana*  
AV556193|AV556193|*Arabidopsis thaliana*  
 30 BE203316|BE203316|EST403338 *KV1 Medicago truncatata*.  
AW649615|AW649615|EST328069 *tomato*  
BE512465|BE512465|946071E06  
BI204917|BI204917|EST522957 *CTOS Lycopersicon esculentum*  
BG590749|BG590749|EST498591  
 35 BG648725|BG648725|EST510344 *HOGA Medicago truncata*  
BG648619|BG648619|EST510238 *HOGA Medicago truncata*  
BG597757|BG597757|EST496435 *cSTS Solanum tuberosa*  
AW221939|AW221939|EST298750 *tomato*  
BE704836|BE704836|Sc01\_  
 40 BG124409|BG124409|EST470055 *tomato*

- BF051954|BF051954|EST437120 tomato  
BG320355|BG320355|Zm03\_05h01\_zea mays  
AV526624|AV526624|Arabidopsis thaliana  
AW933960|AW933960|EST359803 tomato  
 5 AW221278|AW221278|EST297747 tomato  
BE405514|BE405514|WHE1212\_C01\_F02ZS Wheat  
BG314461|BG314461|WHE2495\_A12\_A23ZS Triticum  
BF258673|BF258673|HVSMEF0016G01f Hordeum vulgare  
BG262637|BG262637|WHE0938\_E03\_I06ZS Wheat  
 10 AW030188|AW030188|EST273443 tomato  
BG653580|BG653580|sad76b11.y1 Gm-cl051 Glycine max  
BG319729|BG319729|Zm03\_05h01\_A\_Zm03\_zea mays  
BF053590|BF053590|EST438820 potato  
BE454808|BE454808|HVSMEh0095C03f Hordeum vulgare  
 15 BI075801|BI075801|IP1\_21\_D05.b1\_A002  
BE367593|BE367593|PI1\_9\_F02.b1\_A002 Sorghum bicolor  
2e-074 BF260080|BF260080|HVSMEf0021A22f Hordeum vulgare  
BF627921|BF627921|HVSMEb0006I23f Hordeum vulgare  
BG598491|BG598491|EST503391 cSTS Solanum tuberosa  
 20 AW038168|AW038168|EST279825 tomato  
BG343258|BG343258|HVSMEg0005D23f Hordeum vulgare  
AW925684|AW925684|HVSMEg0005D23 Hordeum vulgare  
BG416093|BG416093|HVSMEk0009L18f Hordeum vulgare  
AW683370|AW683370|NF011C09LF1F1069  
 25 BE420108|BE420108|WWS020.C1R000101 ITEC WWS Wheat  
AW350720|AW350720|GM210009A10F4 Gm-r1021 Glycine max  
AW616564|AW616564|EST322975 L. Hirsutum trichome  
AW011134|AW011134|ST17B03 Pine  
BF630746|BF630746|HVSMEb0013N06f Hordeum vulgare  
 30 AW926045|AW926045|HVSMEg0006C10 Hordeum vulgare  
BE519800|BE519800|HV\_CE0021E12f Hordeum vulgare  
BG343657|BG343657|HVSMEg0006C10f Hordeum vulgare  
BG933682|BG933682|OV1\_16\_C09.b1\_A002  
BE433368|BE433368|EST399897 tomato  
 35 AW219797|AW219797|EST302279 tomato  
BF629324|BF629324|HVSMEb0010N06f Hordeum vulgare  
BE597128|BE597128|PI1\_71\_A07.g1\_A002  
AW220075|AW220075|EST302558 tomato  
AW616639|AW616639|EST323050 L. Hirsutum trichome  
 40 BF645214|BF645214|NF032F11EC1F1094  
AW924540|AW924540|WS1\_70\_H12.b1\_A002

- AI775448|AI775448|EST256548 tomato  
AW983360|AW983360|HVSMEE0010F15f *Hordeum vulgare*  
BF270171|BF270171|GA\_Eb0007B13f *Gossypium arbor.*  
BE919631|BE919631|EST423400 potato  
5 AW037836|AW037836|EST279465 tomato  
BF008781|BF008781|ss79h09.y1 Gm-c1064 *Glycine max*  
BF254651|BF254651|HVSMEE0004K05f *Hordeum vulgare*  
BE599797|BE599797|PI1\_79\_H01.g1\_A002  
BE599026|BE599026|PI1\_86\_E03.g1\_A002  
10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*  
BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*  
AW307218|AW307218|sf54c07.y1 Gm-c1009 *Glycine max*  
AI496325|AI496325|sb05c09.y1 Gm-c1004 *Glycine max*  
AJ277703|2MA277703|*Zea mays*  
15 AL375586|CNS0616P|*Medicago truncatula* EST  
AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*  
BE125918|BE125918|DG1\_59\_F02.b1\_A002  
BF053901|BF053901|EST439131 potato  
BE921389|BE921389|EST425266 potato  
20 BE597551|BE597551|PI1\_71\_A07.b1\_  
BE360092|BE360092|DG1\_61\_C09.b1\_A002  
BE660084|BE660084|491 GmaxSC *Glycine max*  
AJ277702|2MA277702|*Zea mays*
- 25 The invention also relates to modifying SBP/SPL gene or products which represent a family of transcription factors with a bipartite nuclear localization signal (The SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of *Arabidopsis thaliana*, Columbia ecotype). Upon activation  
30 (probably by RKS mediated phosphorylation, the bipartite nuclear localization signal becomes linear and available for the nuclear translocation of the protein. Within the plant nucleus, the transcription factor regulates transcription by interaction with specific promoter elements. In *Arabidopsis*  
35 *thaliana*, this family is represented by at least 16 different members (see following list). In many other plant species, we also identified members of this transcription factor family (See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: <http://www.ub.uni-koeln.de/ediss/archiv/2001/11w1204.pdf>; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

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	name	genetic code
	ATSPL1	At2g47070*
	ATSPL2	At5g43270
	ATSPL3	At2g33810*
25	ATSPL4	At1g53160*
	ATSPL5	At3g15270
	ATSPL6	At1g69170
	ATSPL7	At5g18830
	ATSPL8	At1g02065
30	ATSPL9	At2g42200*
	ATSPL10	At1g27370*
	ATSPL11	At1g27360*
	ATSPL12	At3g60030
	ATSPL13	At5g50570
35	ATSPL14	At1g20980
	ATSPL15	At3g57920
	ATSPL16	At1g76580

\* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5    [AB023037](#)|AB023037|*Arabidopsis thaliana*  
      [BG789832](#)|BG789832|sae56b07.y1 Gm-cl051 *Glycine max*  
      [BG123992](#)|BG123992|EST469638 tomato  
      [BG595750](#)|BG595750|EST494428 cSTS *Solanum tuberosum*  
      [AF370612](#)|AF370612|*Arabidopsis thaliana*
- 10   [BF728335](#)|BF728335|1000060H02.x1 1000 - *Zea mays*  
      [X92079](#)|AMSBP2|*A.majus*  
      [AW331087](#)|AW331087|707047A12.x1 707 - Mixed adult... 128 *zea mays*  
      [AJ011643](#)|ATH011643|*Arabidopsis thaliana*  
      [L34039](#)|RICRMSOA|*Oryza sativa*
- 15   [AJ011638](#)|ATH011638|*Arabidopsis thaliana*  
      [AJ011639](#)|ATH011639|*Arabidopsis thaliana*  
      [AJ132096](#)|ATH132096|*Arabidopsis thaliana*  
      [BF482644](#)|BF482644|WHE2301-2304\_A21\_A21ZS Wheat  
      [BF202242](#)|BF202242|WHE0984\_D01\_G02ZS Wheat
- 20   [BE057470](#)|BE057470|sm58e10.y1 Gm-cl028 *Glycine max*  
      [AJ011628](#)|ATH011628|*Arabidopsis thaliana*  
      [AJ011629](#)|ATH011629|*Arabidopsis thaliana*  
      [AJ011617](#)|ZMA011617|*Zea mays*  
      [AJ011637](#)|ATH011637|*Arabidopsis thaliana*
- 25   [AJ011622](#)|AMA011622|*Antirrhinum majus*  
      [AJ011621](#)|AMA011621|*Antirrhinum majus*  
      [AJ011635](#)|ATH011635|*Arabidopsis thaliana*  
      [AJ011623](#)|AMA011623|*Antirrhinum majus*  
      [BF650908](#)|BF650908|NFO98D09EC1F1076
- 30   [AJ242959](#)|ATH242959|*Arabidopsis thaliana*  
      [Y09427](#)|ATSPL3|*A.thaliana* mRNA  
      [AJ011633](#)|ATH011633|*Arabidopsis thaliana*  
      [AW691786](#)|AW691786|NFO44B06ST1F1000  
      [BE058432](#)|BE058432|sn16a06.y1 Gm-cl016 *Glycine max*
- 35   [AW728623](#)|AW728623|GA\_Ea0017G06 *Gossypium arbore.*  
      [BG442540](#)|BG442540|GA\_Ea0017G06f *Gossypium arbo.*  
      [AJ011626](#)|ATH011626|*Arabidopsis thaliana*  
      [AJ011625](#)|ATH011625|*Arabidopsis thaliana*  
      [AI993858](#)|AI993858|701515182 *A. thaliana*
- 40   [BG593787](#)|BG593787|EST492465 cSTS *Solanum tuberosum*  
      [BF634536](#)|BF634536|NFO60C08DT1F1065 Drought *Medicago*

- BE806499|BE806499|ss59f10.y1 Gm-c1062 *Glycine max*  
AW933950|AW933950|EST359793 tomato  
AC008262|AC008262| *Arabidopsis*  
B28493|B28493|T10A24TF TAMU *Arabidopsis thaliana*  
 5 AJ011644|ATH011644|*Arabidopsis thaliana*  
AC018364|AC018364|*Arabidopsis thaliana*  
AL092429|CNS00VLB|*Arabidopsis thaliana*  
BE435668|BE435668|EST406746 tomato  
BG097153|BG097153|EST461672 potato  
 10 BE440574|BE440574|sp47b09.y1 Gm-c1043 *Glycine max*  
AI443033|AI443033|sa31a08.y1 Gm-c1004 *Glycine max*  
U89496|ZMU89496|*Zea mays* liguleless1  
AW433271|AW433271|sh54g07.y1 Gm-c1015 *Glycine max*  
AW932595|AW932595|EST358438 tomato  
 15 AW096676|AW096676|EST289856 tomato  
AJ011616|ZMA011616|*Zea mays*  
AW036750|AW036750|EST252139 tomato  
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*  
AJ011614|ZMA011614|*Zea mays*  
 20 AJ011642|ATH011642|*Arabidopsis thaliana*  
BE022435|BE022435|sm85h04.y1 Gm-c1015 *Glycine max*  
X92369|RMSPB1|*A.majus*  
AC015450|AC015450|*Arabidopsis thaliana*  
AC079692|AC079692|*Arabidopsis thaliana*  
 25 AJ011632|ATH011632|*Arabidopsis thaliana*  
AJ011631|ATH011631|*Arabidopsis thaliana*  
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*  
AJ242960|ATH242960|*Arabidopsis thaliana*  
AJ011610|ATH011610|*Arabidopsis thaliana*  
 30 AJ132097|ATH132097|*Arabidopsis thaliana*  
AL138658|ATT209|*Arabidopsis thaliana*  
AJ011615|ZMA011615|*Zea mays*  
BE499739|BE499739|WHE0975\_ Wheat  
AW398794|AW398794|EST309294 *L. pennellii*  
 35 AJ011618|ZMA011618|*Zea mays*  
AW747167|AW747167|WS1\_66\_F11.b1\_  
AJ011577|ATH011577|*Arabidopsis thaliana*  
AI992727|AI992727|701493410 *A. thaliana*  
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*  
 40 BE804992|BE804992|ss34h10.y1 Gm-c1061 *Glycine max*  
BE325341|BE325341|NF120H09ST1F1009



- AC007369|AC007369|*Arabidopsis thaliana*  
AJ011619|ZMA011619|*Zea mays*  
BI099345|BI099345|IP1\_37\_H10.b1\_A002  
BI071295|BI071295|C054P790 *Populus*  
 5 A2920400|A2920400|1006019G01.y2 1006 -  
A2919034|A2919034|1006013G02.x3 1006 -  
BE805023|BE805023|ss35d09.y1 Gm-cl061 *Glycine max*  
BG582086|BG582086|EST483824 GVN *Medicago truncata*  
AJ011609|ATH011609|*Arabidopsis thaliana*  
 10 BE023083|BE023083|sm90e08.y1 Gm-cl015 *Glycine max*

Furthermore, the invention relates to modifying NDR-NHL-genes or gene products. All proteins belonging to this family contain one (and sometimes even more than one) transmembrane domain. *Arabidopsis* contains a large number of NDR-NHL genes, such as:

- aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),  
 aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,  
 aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, al163812,  
 20 f20d21-35, t13ml1-12, fl1e22-7, t23g18, f5d14-4266, t32f12-16, fl1f19-11,  
 fl1f19-12, fl1f19-13, t20p8-13, fl2k2, f23h14, k10d20-44043,  
 k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-80,  
 t25p22-30, mhfl5-4, mhfl5-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-9667,  
 fl4f18-60, At1g17620 F11A6, At5g11890, At2g27080, At5g36970,  
 25 mlf18, At1g65690 F1E22, At4g01110 F2N1, At2g35980 fl1f19,  
 At4g01410 F3D13, At1g54540 F20D21, At2g46300 t3f17, At5g21130,  
 At3g11650 T19F11, At5g06320 MHF15, At5g06330 MHF15, At2g01080  
 fl5b18, At2g35460 t32f12, At2g27260 fl2k2, At2g35970 fl1f19,  
 At5g53730 MGN6, At5g22870 MRN17, At4g09590, At3g54200, At1g08160  
 30 T6D22, At5g22200, At3g52470, At2g35960 fl1f19, At3g52460,  
 At5g56050 MDA7, At3g20590 K10D20, At1g61760 T13M11, At3g20600  
 K10D20, At1g13050 F3F19, At3g11660 T19F11, At3g44220, At1g64450  
 F1N19, At3g26350 F20C19 C, At4g05220, At5g45320 K9E15,  
 At4g23930, At4g13270, At4g39740, At1g45688 F2G19 W, At5g42860  
 35 MBD2, At1g32270 F27G20, At4g30660, At2g45430 f4123, At4g30650,  
 At1g69500 F10D13

and

- 40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

- At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,  
 At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,  
 At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,  
 At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,  
 5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,  
 NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,  
 At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,  
 At4g26820
- 10 NDR-NHL genes belong to a large family of which one of the  
 first identified is the defence-associated gene HIN1 (Harpin-  
 induced gene). HIN1 is transcriptionally induced by harpins  
 and bacteria, that elicit hypersensitive responses in tobacco.  
 It is thus believed that the genes of the invention also play  
 15 a role in the hypersensitive reaction. Especially (see also  
 chapter 8) since the genes of the invention bear relation to  
 brassinoid-like responses and since brassinoid pathway  
 compounds have been found to interact in this same defence  
 system in plants. Other plant species also contain members of  
 20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

- 25 BG582276|BG582276|EST484016 GVN *Medicago truncata*  
AV553539|AV553539|*Arabidopsis thaliana*  
AC069325|AC069325|*Arabidopsis thaliana*  
AV526693|AV526693|*Arabidopsis thaliana*  
BG583456|BG583456|EST485208 GVN *Medicago truncata*  
 30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*  
BE997791|BE997791|EST429514 GVSN *Medicago truncata*  
BG580928|BG580928|EST482657 GVN *Medicago truncata*  
BF520916|BF520916|EST458389 DSIL *Medicago truncata*  
AV544651|AV544651|*Arabidopsis thaliana*  
 35 AV543762|AV543762|*Arabidopsis thaliana*  
AW559665|AW559665|EST314777 DSIR *Medicago truncata*  
BG581012|BG581012|EST482741 GVN *Medicago truncata*  
AV552164|AV552164|*Arabidopsis thaliana*  
BE999881|BE999881|EST431604 GVSN *Medicago truncata*  
 40 AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*  
AW219286|AW219286|EST301768 tomato  
BE124562|BE124562|EST393597 *GVN Medicago truncata*  
AV540371|AV540371|*Arabidopsis thaliana*  
 5 AV539549|AV539549|*Arabidopsis thaliana*  
BG647432|BG647432|EST509051 *HOGA Medicago truncata*  
BE434210|BE434210|EST405288 tomato  
BG725849|BG725849|sae42g02.y1 Gm-cl051 *Glycine max*  
AP003247|AP003247|*Oryza sativa*  
 10 BE348073|BE348073|spl1a11.y1 Gm-cl042 *Glycine max*  
AW508383|AW508383|si40c06.y1 Gm-r1030 *Glycine max*  
AI856504|AI856504|sb40b07.y1 Gm-cl014 *Glycine max*  
BE556317|BE556317|sq01b07.y1 Gm-cl045 *Glycine max*  
AA713120|AA713120|32681 *Arabidopsis*  
 15 AV541531|AV541531|*Arabidopsis thaliana*  
AI894456|AI894456|EST263911 tomato  
AW704493|AW704493|sk53g11.y1 Gm-cl019 *Glycine max*  
AW219298|AW219298|EST301780 tomato  
BF425685|BF425685|ss03c11.y1 Gm-cl047 *Glycine max*  
 20 AV422557|AV422557|*Lotus japonicus*  
BE190816|BE190816|sn79a08.y1 Gm-cl038 *Glycine max*  
BG580331|BG580331|EST482056 *GVN Medicago truncata*  
AV423251|AV423251|*Lotus japonicus*  
AI896088|AI896088|EST265531 tomato  
 25 AV413427|AV413427|*Lotus japonicus*  
AV426656|AV426656|*Lotus japonicus*  
AV416256|AV416256|*Lotus japonicus*  
AL385732|CNS0690I|*Medicago truncatula*  
AB016877|AB016877|*Arabidopsis thaliana*  
 30 AV419449|AV419449|*Lotus japonicus*  
AI486269|AI486269|EST244590 tomato  
AV411690|AV411690|*Lotus japonicus*  
AV419925|AV419925|*Lotus japonicus*  
AV418222|AV418222|*Lotus japonicus*  
 35 AV409427|AV409427|*Lotus japonicus*  
AC005287|AC005287|*Arabidopsis thaliana*  
AV426716|AV426716|*Lotus japonicus*  
AV411791|AV411791|*Lotus japonicus*  
BG351730|BG351730|131E12 Mature tuber  
 40 BG046452|BG046452|saa54b12.y1 Gm-cl060 *Glycine max*  
AI781777|AI781777|EST262656 tomato

- BE451428|BE451428|EST402316 tomato  
AI772944|AI772944|EST254044 tomato  
AI895510|AI895510|EST264953 tomato  
AW030762|AW030762|EST274017 tomato  
5 AW218859|AW218859|EST301341 tomato  
BE203936|BE203936|EST396612 KV0 *Medicago truncata*  
AV410289|AV410289|*Lotus japonicus*  
AW032019|AW032019|EST275473 tomato  
AW030868|AW030868|EST274158 tomato  
10 AV421824|AV421824|*Lotus japonicus*  
BG646408|BG646408|EST508027 HOGA *Medicago truncata*  
AF325013|AF325013|*Arabidopsis thaliana*  
AC007234|AC007234|*Arabidopsis thaliana*  
AW217237|AW217237|EST295951 tomato  
15 AC034257|AC034257|*Arabidopsis thaliana*  
AW625608|AW625608|EST319515 tomato  
AW031064|AW031064|EST274371 tomato  
AF370332|AF370332|*Arabidopsis thaliana*  
AB006700|AB006700|*Arabidopsis thaliana*  
20 AW035467|AW035467|EST281205 tomato  
AL163812|ATF14F18|*Arabidopsis thaliana*  
AI896652|AI896652|EST266095 tomato  
AI730803|AI730803|BNLGH17970 Cotton  
AW034775|AW034775|EST278811 tomato  
25

- The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex)
- 30 comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying
- 35 expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and NDR0/NHL28 and members of the SBP/SPL family. Here we show
- 40 that in vivo the individual components of this signaling

complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products  
5 are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore  
10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing  
15 complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane  
20 towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of  
25 such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the  
30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes  
35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying

- 5 teh brassinosteroid pathway can, amongst others, be found in: Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-713, genetic evidence for an essential role of brassinosteroids in plant development; J. Cell Biochem Suppl. 21a 479 (1995) ; Mandava 1988 Plant growth-promoting  
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol. 39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66; Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol. Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-  
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory, that modification of the RKS genes will result in a modification of the brassinosteroid pathway, thereby giving the various phenotypes that are shown below.

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- "Functionally equivalent" as used herein is not only used to identify the functional equivalence of otherwise not so homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins, but also means an equivalent gene or gene product of  
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in *Arabidopsis Thaliana*, e.g. identifying a homologue found in nature in other plants or a homologue comprising a deliberate nucleic acid modification, such as a deletion, truncation, insertion, or deliberate codon substitution which may be made on  
30 the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. Homology is generally over at least 50% of the full-length of the relevant sequence shown herein. As is well-understood,  
35 homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating



- cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,
- 5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant
- 10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.
- 15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery
- 20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides
- 25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and
- 30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an
- 35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

5

In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

35

regeneration capacity of in vitro cultured *Arabidopsis* callus.

Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem.

Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

- In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired.
- Especially when the number of revertants (growing normal pollen) is extremely low.
- Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.
- Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses

10 with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10

15 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment,

20 *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is

25 prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene

30 products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.



Table 1

Homology between members of the syntaxin family and the NDR  
NHL family

- 5 NHL10= At2g35980  
maaeqplnga fygpsvpppa pkgyyrrghg rgcgccllsl fvkviisliw ilgvaalifw  
livrpraikf hvtdasltrf dhtspdnrlr ynlaltvpvr npnkriglyy drieahayye  
gkrfstittlr pfyqghkntt vltptfqgqn lvifnagqsr tlnaerisgw ynieikfrlr  
vrfklgdldkf rrikpkvdc dlrplstsn gttttstvf ikcdfd (SEQ ID NO:1)
- 10 Atlg32270 syntaxin,  
MVRSDVKEQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNQ  
RLGAVPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYR IDVKLSINFR  
VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKKMLLI GQLVKDTSAN LREASETDHR
- 15 RDVAQSKKIA DAKLAKDFA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS  
QEQRVLMEGR RQEI VLLDNE ISLNEARIEA REQIQEVKH QISEVMEMFK DLAVMVDHGG  
TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLFFFLFSG DLCRCVCVGS  
ENPRNLNPTRR KAWCEEDEE QRRKQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK\* (SEQ ID NO: 2)
- 20 Below the homology is shown between NHL10 (Upper line) and a  
syntaxin protein. (bottom line). The identical amino acids are  
shown in the middle line.
- 25 IVRPRAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPKNRIGLYYDRIEAHAYYEG  
VR KF V DA LT FD S N L Y L L RN IG YDR EA YY  
MVRSDVKEQVYDAELTHFDLESNNN-LQYSLSLNLSIRNSKSSIGIHYDRFEATVYYMN
- 30 KRFSTITLTPFYQGHKNTTVLTPTFQGNLVIFNAGQSRTLNAERISGVYIEIKFRLRV  
R FY G KNT L F GQ LV GVI I K  
QLRGAVPMPFLFYLGSKNTMLLRALFEGQTLVLLKGNERKKFEDDQKTGVYRIDVKLSINF
- 35 RFKLGDLKFRRIKPKVDCDDRLRLPLSTNGTTT  
R L KP V C L PL T  
RVMVLHLVTWPMKPVVRCH-LKIPLALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

[http://mips.gsf.de/proj/thal/db/search/search\\_frame.html](http://mips.gsf.de/proj/thal/db/search/search_frame.html)

- 5 searching for homologous sequences with the sequence Atlg32270

	gene code:	predicted function:
	Atlg32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein	Syntaxin
	AtVam3p (gb AAC49823.1)	
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	Atlg65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein	Syntaxin
	AtSNAP33	
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	Atlg61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	Atlg61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	Atlg54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1gl1250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5g42860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin
35		

40 This observation provides the explanation for understanding  
the mechanism by which the RKS / NDR-NHL complex functions.  
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

- 5        Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and
- 10        allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible
- 15        as a monomer or a (hetero)dimerizing molecule binds the transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.
- 20        One class of ligands interacting with the RKS and / or ELS receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5' - towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5' - and trailer sequences 3' -) are indicated in small letters.

Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence

The second (set of) lines represents the pro-peptide.

The last line represents the conserved Cysteine motif.

**A. Atlg22690**

15           1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttctctcat  
           61 ctatctctct cagtgctaca atgtctgaac taagagacag cgtgaacta tcatthaagc  
           121 ataaactacc aaagtatcaa gctaagttaa aaatctctct catctccacg taacaaattg  
           181 agtagcttia agatattagt gaactaggt tgaattttc tttctctct tcaacgcatc  
 20           241 ctccgaaaaa agggagacaa tcaaaactgt ttgcatatca aactcaacaa ctttacagca  
           301 aatgcaatct ataactctgt attattccaa taasaaactg tgattatgt ttggtccag  
           361 cgaatgaagt ctatgcatgt gatctctatc caacatagtg aattgttcag aaataaaaa  
           421 gtatctgaaa tgtatctata taagaatca tccacaagta ctattttoc acactacttc  
 25           481 aaatcacta ctcsagaaat ATGAGAGAGA TGAATGTGGT GGCTTTGTT AGCCTGATCA  
           541 TCTCTTTCT TCTGTTTCT CAGTAACT gttaaacaa ttttcaagc tacctttct  
           601 ctatttcaga caaaccaaaag taasaaactg aaaaactctc ctggcttttc atagGTACTT  
           661 GCAGAGTTG CATCATCCAG CAACATGAA ACTTCTCTG TTTCTCAGt aagagtgata  
           721 caaaacata ctaaacaaac tttaagaga gtaatatata agaaatgtt ggcttctttt  
 30           781 tttgtttgct aatcagaCGA ATGACGAGAA CCAAACTGCG GGTTTAAGA GACATATCCA  
           841 CCAATGTTCA AGAATCagtt agtctactct ttcaacactc taactctttt gtcttaagta  
           901 ttttttttgc ccccacaaac ctttttttta ttaastgagc aaattttat agATTGGGG  
           961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTGTGCA CAGAGCCTGT  
           1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CGCGGGGAA CCTCGGCAA CACASCATCA  
 35           1081 TGTCTTGTCT AGGCCAGTAT CGGTACATCT GGCAATAAAG TCAAAATGTC TTAAsagact  
           1141 tctcatttct caactatagt ctcactctct gattatgttt ctctctttgt tatgttgcac  
           1201 gtgtgatgtg tyagcttatt attatgttga ttgttgcac aatcaacata tataattgt  
           1261 atcgattccy atcaataaga tgaagtattt tatggcttat taagtttttt tttttttttt  
           1321 ttgggcacaa tggctattaa gttttaaaca totgatitta ttggttacaa aaacaacaaa  
           1381 agtttcattt tcatattaac acaaaactct catcatatt accaaacaaa aaaaatacac  
 40           1441 aagggggaga gaggacaaag gtctcttggt cagagtttgc atctgtttg agccgtcac  
           1501 gttctcttag cttaacagcc acacacactt tataaagctt cagcgcgac ttcaacgcac  
           1561 ctgcgcgggg ccgagccacc ttatgtttg gatcaacaa caaaacttct tcaaacgcac  
           1621 tcaatgccaa aggc (SEQ ID NO: 3)

45   MKKANVVAEVLIIISFLLSQVLA  
      ELSSSSNNETSSVSQTNDENQTAAFKRTYHHRPRIN  
      CGHACARRCSKTSRKVKCHRACGCCAKCQCVFPPTSGNTASCFCYASIRTHGNLKCPC\* (SEQ ID NO: 4)

50

**B. At1g74670**

1 gaaaaaaga agaaaagata atggtccgta ttaataagat tgaaaacttg aaactacttt  
 5 61 ttagtttgta tataatacac tagacteggy atccagttga gttctcttct ttattttgag  
 121 ttgtgtggtta tgtttgattt tagcttttta tatgtaata agatatttta cgaattatgg  
 181 ttctatttgg gtageagttg tagaattgct taacaacata agtgacgaga tgaagataat  
 241 aaagtataat aatatafgta ccgttattaa ctattgtatc atgtgaatga ggaagcttac  
 301 acacacacac ctctctaaas tagctgacaa aactggttgt tacacacaac acatctatac  
 10 361 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atctctcttc  
 421 tctctcaaga gctagtcatg GCCAACTCA TAACTTCTTT TCTCTTACTC ACAATTTTAT  
 481 TCACTTTCGT TTGTCTCAGT ATGTCAAAAG AAGCTGAGTA CCATCCAGAA AGTgttaagtt  
 541 ttattttttt ggtaaatag aagtgtaag ttittataat catcaaatg tttttgcctt  
 601 tccctttcta ttatttgcta taaatcatac acccggtta aaaktgtttt tgaattataa  
 15 661 cagtATGGAC CAGGAAGTCT GAAATCATAC Ogtaaataa aactctctct tcttttatga  
 721 atcttggttc ttattatata tcaaatataa actcgattat catgattgca gAATGTGGAG  
 781 GACAATGCAC AAGGAGATGT AGCAGCACAA AGTATCATAA GCCATGCATG TTCTTCTGOC  
 841 AAAAGTGTG TGCTAAATGC CTTTGTGTTC CTCAGGCGAC GTACGGCGAC AAACAAGTGT  
 901 GTCTTGTGTA CACACACTGG AAGACTGAC AAGGTGGACC AATAGTCCA TAAacaaaa  
 961 catgagaga gaaccccaas cctgtttcct attttatata attatttcaa gtatgctttt  
 20 1021 gttgtcgtga tggtttaatt atagtgtttt tgcaggtatc atttatcatc gataaacaat  
 1081 atcatataaa atctctatg ttctcttcac gttttgttcc ttttgttgta gtcaatacac  
 1141 gaaatgtga tggacctctc aattaggaat atataaaatt ttatttata attagataat  
 25 1201 ctittcgtata gttaaaattc caaggattac ttttgattcg ttggggacaa tctattttat  
 1261 attttacttt ctasgtttgt ataactatac cttaaaagt tttagcagag tctaatgct  
 1321 tttagataaa ttgtactat ctagttaagc ttccgaaaat tgaactttt ccaaaaggtg  
 1381 ctatatcaat ttgattcaat aatbycgct tctctctagt tttttacaa tagggagatt  
 1441 tttagacgat gat (SEQ ID NO: 5)

MAKLITSFLLLTILFTFVCLTMS

KEAEYHPESYGGPSLKSQY

CGGQCTRRCSNTKYHKPCMFQCQKCCAKCLVFPSTYGNKQVPCYNINWRTQGGPKCP \* (SEQ ID NO: 6)

C. At1g75750

1 cacaactttt atagcaacca ccaaacggacc cattttgaaa aagagaaaaa aaaccacaaa  
 5 61 aacacacata aataatatgc tgataacaat gtcttaaaaa tcatattacc attctatgta  
 121 atcaatatct attgcaaaaa atattatata gaatacaaat gaataaatgt aaatacacia  
 181 tgattttctca attaactaaa aaataataaaa atgtcttact ttattttcag caactgtttg  
 241 aaagtacttg caatcatatc gtattttgaa ttataaaact cagaaacaat tattttccct  
 301 gaaaagttaa aacttttaatt aagatattta taataataaaa agaatagtct agacgcaaaa  
 10 361 tgggggtcgt gtgtccatoca aaggagtgtc ataaatagaa cctccaagt tctcatatag  
 421 aacacacacac taataaacaca ttatcatata cagtctgatt tgagctaagt tctctcatca  
 481 taactctc tttgagaatc atggcatttt caaaagctct tctgctctt cttctcatat  
 541 cttctcttgt tctctcactc ctccggcctg atgtcgtaac tcttttctat cacaacttaa  
 601 ttatactcaa tataatactt atgttttcaa aaacatattt ctccatgttt acaacaatat  
 15 661 tcttgcaaga aaactcacag aagaaaaatg gttacgcata gaagatcgtt aattatatga  
 721 tttttattaa acctaacgtt aaatttagag tgagattaat aatctgtgtt tttctttctt  
 781 gtatatatag attgtgggag tgcgtgtgta gcacggtgca gactttcgag gagcccgagg  
 841 ctgtgtcaca gagcgtgctg gacttgcctg tacaggtgca actgtgctc tccgggacac  
 901 tacggaatct acgcaaatg ccagtgcctc gcttgcctca cctccacgag tcgaagccgc  
 20 961 aagtgcctat aagaagaac aaagctctta attgtcggg ataagtggac gatgtcgttt  
 1021 tgttagtatt cactttggcg tatatatgtg gatcgataa taacagagaa ggtacgttgt  
 1081 cgttgtgagt gtgagtactg tatatttaat ggttctattt gtttttactt gcaagttttc  
 1141 ttgttttgaa ttgttttttt tcatatttgt atatcgattc gtgcattatt gtatttcttc  
 1201 aatttgtaat aagatatgt tacttttgag tggttgttta tcatatttt ttcttatggt  
 25 1261 aaggagtgtt ggaagaatc cgaagatgat atataaagta atttgatat cgaagcaaga  
 1321 tgataactac tagactagct gagtataaga atattgatgt atatattgc ggaactttt  
 1381 gaatttatta taccattatt taatcacgac catataaana taattctgtt ttgcgttata  
 1441 atttgtgtta atacgataga gtacacaat ga (SEQ ID NO: 7)

MAISKALIASLLISLVLQLVQA

DVENSQKNGYAKKID

CGSACVARCLSRRLCHRAAGTCCYRCNCVFPCTGYNDKQCQYASLTHGGRRKCP\* (SEQ ID NO: 8)

D. At2g14900

1 ataactaaca atggttgagt gggagatgfc ttttagtcaa gtggttaast atatttgact  
 5 61 tegttttttt cattggagtt tgactctact aagttgtgtt toctcgcgta gtaagaattg  
 121 gttatggatt agaccgatac gactctaaag tglcaaagaa aaaaastgtt gytgtgttga  
 181 agtaaatatg tagattgtgg gpgattaaag tatgtttga ttcaactcat tatgtttatt  
 241 ttttcatgaa ttctaaatgt aaagtcttca taactcttatg ttacttttta caaattgtaa  
 301 ggaattactct gaatttttgt atcgattctc aagcaaaata caaataaca atgactgaac  
 10 361 aagttgataa aacataatgg aaggaataat actgcaactc tattaataac taaagaagtt  
 421 ggtagattgg cctataaaag gagaataaag agacacaaag aaggtctatt attcggggag  
 481 taagaagaag caaagaanaac ATGAAATAA TAGCTCCAT CTTAGTGTTA GCCTCTCTTC  
 541 TTTCTATCAG TTCACTCTT GCTTCGGCTA CTATATCAG ttggtttcaa tctcttcaag  
 601 aatcttcttc tctctatttt tttttctctc ataaagttag ttatgttatg attggtttag  
 15 661 gtcaaatg ttcttttatg ctttcttttc cataaanaa atattacaaa tattaactag  
 721 aacaacataa catgcaaacg agtaatacaa aatctattat tatgatcaaa acaatcatga  
 781 attagttgga cttatttgtt aaatccgaa aactcacta aataaagtg aactctact  
 841 acatggtctt agacgcaaaa cttttaaggg tatctacaca agtttggaat gaataatttc  
 901 ttgcatgggt agtgtagaag gatctagaag atccacaaga tcaatagtgt atctctaaag  
 20 961 tctttttaca ttgagaagtg aggaatatatt tgttgtatta gaagaattta tagtgaaatg  
 1021 aattttttaa ctatgtacga tcaattatat acgatacttt tattaaggaat ctgtggatc  
 1081 ttctagATGC TTTTGTAGT GGCGGGTAG CTCCGCCACC GCAGAGCAAA GATGGACCG  
 1141 CTTTAGAGAA ATGCTGTGGA CAGAAATGTG AAGGGAGATG CAAGAAGCG GGGATGAAG  
 1201 ATCGGTCTTT GAAGTATTGT GGGATATGTT GCAAGACTG TCAAGTGTTT CCTTCAGCA  
 25 1261 CTATTGGGAA TAGAGCAGAA TGTGCTTGCT ATCGTGACAA GCTCAGTAC AAGGCCATC  
 1321 CTAAATGTCC TTGATctcat tctttccaa ccaaaatttt aaataaatga atgaagaga  
 1381 tccagtaaac taataataaa ctataaatgg actctttgtt tatgtatttt ttttttcat  
 1441 tctcattttt acgaatttgt ctggtctctt ttgaagtaag tttttaataa ttgaaaagtg  
 30 1501 ctaaaattat gtggaatcgy ataatgttaa tgaatgatat aatatataag tcoctagttt  
 1561 ttgtaagaana cttgaatata aataatttt catcaaatat aataataana tatattgtat  
 1621 aattagattg gctcaacgaa catacaaat tgaatgatat tttttctct aatatattaa  
 1681 tcatccaast ttgtattgtg ccaatgaag agatggttat gaggactaga agatagaag  
 1741 gagaagaacg tgtttggtaa nataattatg atggagttga gacaactttt aagagatttt  
 35 1801 aaaaagactg actaacgtgt taggttcatc aagt (SEQ ID NO: 9)

MKIIVSILVLASLLLISSSLASATIS

DAFGSGAVAPAPQSKDGPALKW

40 CGQKCEGRCKEAGMKDRCLKYOGICCKDCQCVFSGTYGNKHECACYRDKLSKSGTKPCP\* (SEQ ID NO: 10)



E. At2g18420

1 gccaatgggt aactgaggea gaaggataag acccaaaaaa aaactaaaaa ggacagattg  
 5 61 aattagtaaa aagtaaat ctaaaaaccg aaacaaatct taagttgggt tatatactc  
 121 tgcattgacc aacaaagaa agtagactga aatttattg aaaaigactc tglaaaggca  
 181 tattatataat ttaatttagg aatgaatgt taantccttt aattgtttt gatttcaca  
 241 aaggataaag aatatgtgt tacatactc ttaattgttt gaccaaaaaa ataaaaatgt  
 301 gataagaanaa aataaaacca ttttgacca agttcttata gttttaatat tttttaattg  
 10 361 tcatttgtta gtactaata atattacatt aaactcaatg tataaataga agccccattc  
 421 tctacgcttt tataattagc acaaccaa aaacttcatt tgcattttg tctcctcttt  
 481 tgtttctctc gatcactagt ATGGCTGTAT TCGAGCTCTT GCTTCTCTCT CTCTCATAT  
 541 CTCTCTCTGT CCTCGACTTC GTCCATGCGG ATATGCTGTg caaattttaa caaccaata  
 601 tattttctta tttagtttta ttttttca acttttgtct acgttctaag ggaatttttt  
 15 661 tcaaaatatt catgcagACG TCGAATGACG CCGTAATAT CGtaataac tctatcatat  
 721 aaacacgtac gttgaatttc tatatactgt tgtttaattg aagttttgt tgsaanttgt  
 781 atgtatttgt agattgcaac agcaggtgcc aagagCGGTG CAGTCTTTCG AGTAGGCCAA  
 841 ATCTTTTGTCA CAGAGCTGTC GGGACTTGCT GCGTAGCTG CAACTGCGTG GCACCGGCCA  
 901 CATCGCGAAA CTACGACABA TGTCCGTGCT ATGTAGCTT AACCACTCAC GGAGGACGCA  
 20 961 GAAAGTGTCG Taaaaaactc tgcgtgttt tgaattgatg tgtttataa taacttact  
 1021 ttatgagagt aattgtggtt attttctg gaattataa aaagcaaaag aaaggaatg  
 1081 ttatacgcta tgtgcaactc ttgatcttt gttttagtgt ttatccaatt tgaactgtt  
 1141 gggttggttc ctggttaaca ttaggcttga aaaggtattg tttttatta tacaattcac  
 1201 taatatggca tgcctctgtc atataaata aagaatgaag agagaagtaa aagagtttcc  
 25 1261 tttttttact catggaagt aggcattggt tttaaatg gtaacacag aattgaggag  
 1321 gacttaataa actatgacct aaactgaga gcgattgat atgtaacgtt accaacaata  
 1381 ccaataaata tatgaagaat agtatatgaa attacgtta attaattgtt ccggttgaa  
 1441 tgaattatat atagaagtaa cagtacgatt ttattacat tttgtacaa gattcctaga  
 1501 aaggtataac ctctataaag ttaataatg tcttgactct tgactcttc aggcataata  
 30 1561 attcacggca taattaatgc ttcaactatt attctatat ctatataca tgaattccaa  
 1621 caaagaagc ataatatca tcttaacag tatctgcag tgaattgaa catattcaac  
 1681 atcaaacagg acaaaaaagc aagataccgt cgaacactc aaaccccatg tatcataac  
 1741 tccactcttc tctttcttaa attcccggtc gttgcacaa tc (SEQ ID NO: 11)

35 MAVFRVLLASLLISLIVLDFVHA  
 DMVTSNDAPKID  
 CNSRCQERCSLSSRPNLCHRACGTCCARCNCVAPGTSGNYDKPCFYGSLTTHGGRKCP\* (SEQ ID NO: 12)

40

**F. At2g30810**

1 cttttatttg ttgtgaaaa aaacaastag cttttatttg tcttaggaat tatttaatag  
 5 61 attaaataac agctattttt cttctatttc ttagttagta aatatattaa aatcagacc  
 121 aaaattaati gtttatgtta atatatattac tctctaatcc ttlatattaa aatgtataa  
 181 tgcctgtagt taataaattg ttttccaaaa ttcattcata attttattcc taaattattt  
 241 tggccaagaa aacacatctt tgaataatta aatgcttctt tgtatttgat aattcttga  
 10 301 tatttttaaa tacctcttat actatgcca tcttatttgg tataaatagg tttaacattg  
 361 atcttgaaat atctcctaag aaactcaaaa gigaataag agatcaaat GTTAAAGCTC  
 421 ATAGTGTGCT TGTGTATATC CAGTTGTGTG TTGCTACTC AATTTCTAA Tgtaaaat  
 481 attattattt tcttcattat atgatttatg aattcagaga aataaagttt tttttttat  
 541 gtgtgtatgt acaggGTGAT GAATTAGAGA GTCAGCTCA AGCAGCTGCA ATCCATRAAG  
 601 tatatttaaa ttataaata tcaaatactg aataataaet aataaatata ttacaacaag  
 15 661 aatctcaatg ttatttttca aactacataa ttttaaaata ttttatgtat aacacaatg  
 721 tatattatta tgcctccat tgaatttgat tctaaatttg tttttgttat ccaaccaatt  
 781 tcsgrATGGA GGAGAGGCT CACTTAMCC AGAAGttaa ttgtctaaaa gatattattt  
 841 ttatttttat agtaaatgat tgcataatc aactactaaa taatttattt gttgatttat  
 901 attttctga agAATGTCCA AAGCATGTG AATATGATG TTGGGCGACA TCTCACGGA  
 20 961 AACCATGTT GTTTTTTGC AACAAATGTT GTACAAATG TTTGTGTGA CCATCGGGA  
 1021 CATATGGACA CAAGAAGAA TGTCTTCTT ACAATAATG GACGACCAA GAAGTGGAC  
 1081 CAAAATGTCC ATGaaacaa aaasttgytaa asgcaaaata aaatctatgt ttgttatctc  
 1141 tcaataaaat ctatgtttgt aatccttgtt ttctaatata gaataataa tggagtttcc  
 1201 taatttctt ctatgcaga atcaaatgta atgcacaaat aaatigaagg gacttggacc  
 25 1261 ttttctgta agttctttct ttaaatcaag aaatatttg attataattt tcaacttca  
 1321 aaacacaaaa catgtatgct ctttaacctc catccaaaca aatgcattt ctctcttct  
 1381 ttttcaaac atttcaaac aatctccat attatatca agatatatga tottttaaa  
 1441 ttgaatttat ttaggccatg ttttaaatc gtgtttggtt agattgacct atgaattgt  
 1501 gacatatttt aacattccta aatatgacta aaatgatta aagatattta ataatatatt  
 30 1561 tgcctatta aaatgatta aataaataa ata (SEQ ID NO: 13)

**MMKLIVFVFISSLLFATQFSNG**

35 **DELESQAQAPAIHKNGGEGSLKPEE**

**CPKACEYRCSATSHRKPLFFCNKCNKCLVPSGTYGHKECPCYNNWTTKEGGPKCP\*** (SEQ ID NO: 14)

40

G. At2g39540

1 taatgctata cttttaatct ataataata ttapagtga ctttaagaaat ttcaaatagt  
 61 atacaataa ataaaaatga starttgta gtgtacaaa ctygtgtca taatcatcat  
 121 tcatcaggat ttcaaaaata tctcaaaatt gttgtaagtt catgtaattc gaataagaatg  
 181 tgacactataa gaataaatt tacaatttaa aaatgcttc aatctggtt acaaaaaaaa  
 241 ctttcaatac tagtattata ctactactt agtcaaaaaa gtttatgaat atggtttttt  
 301 ctgtatgita atsttttaa ctgaaaatag taccgacata acaagtaag atatctttat  
 361 ttaagtaaac aaacattaat ttcccttcaa atcttccata ttaaggattc ctctctttgt  
 421 agcacattt caccatcat acctgtgttt cgcatactt taaatttgt atcgtagca  
 481 aactcttcy agaacaag ATGAAGCTCG TGGTTGTACA ATCTTCATA ATCTCTCTC  
 541 TCTCACAATC TTCTTTTCT GTACTTTCAA GTGCTGATTC GTgtaagtg ttacttaac  
 601 tagttaataa ttgtaggtca tgcattgac attttgaac aagttttctg aaattctaag  
 661 attttacata tatatgtgat aaatgaatta gcagCATGCG GTGGAAAGTG CAATGTGAGA  
 721 TGCTCAAGGG CAGGACAMCA TGAAAGATGC CTCAGTACT GCATATATG TTGCCAGAG  
 781 TGTAAATGAG TTCTTCGGG AMCTTTCGA CACAAAGATG AATGTCCTG CTACCTGAT  
 841 ATGAAMCT CAAAGGTG ATCAAATGT CCTGAAGct tctttgaaga tctctatcac  
 901 atacataaa cttctscyta ctatatgtgt ggaatatata atcacattct atgtttgaaa  
 961 tatataaaat aaatcaatg ccccaatgt tggaaatctt caatgtgata tcttaataa  
 1021 tatacgaat aaaaagttt aaattttca atctctttt taacttttaa tcttaattct  
 1081 taacacatca acgaatcttt aatctttaa catgtagata attatcagag caactsaaca  
 1141 ttgcgcggtt ttgtgattat acaagtaac atcgtgctgt tttagactt tgaaaaccac  
 1201 agatcaaaa actgttact ttctcttaag agaagcaaa gcgcgtgag tccaaagag  
 1261 tttagagaga tctgttgact cactaccga gaacagcgt atgtcagaga ccgcgtgtc  
 25 1321 aatcgattcy gaccgatcta agtcggagga agaagacgaa gaagagtatt ctccac (SEQ ID NO: 15)

MKLVVVQFFIISLLLTSSFSVLSSA

DSS

CGGKCNVRCsKAGQHEELKYCNICCGKCNVPSGTFGHKDECPCYRDMKNSKGGSKCP\* (SEQ ID NO: 16)

35

H. At3g02885 (GASA5)

5           1 cgctttctat tacacttttt ttctctttta gtgcgacttc acaattagct taatttaatt  
           61 cctaaactcg ctattttctt cctttctata taagatattt alcaattagtg acattttcat  
           121 ttctccaaaca gagcgtttag acactagtes actacacaaat ataattttcc aattttcaat  
           181 gagagaaatg tttttttttt tttttttcca gccaagattt tagtcttttg gtctctctata  
 10          241 cgtgggtaat tagtgattag taattttacac tgttgagctc ttgacattgt ctaagagaca  
           301 aaaacgacaa gtgtggtacg taattagaaan ttaaaatgac ctacttcccc agaatacagj  
           361 catgaacatt ggcacatcca aettttctga ataccattga aggaatcca cactaatcat  
           421 ttctcttata aatattcttta atccgtttta ttgttctcta agaatcatte attggaatc  
           481 asgatttttt aaccsaaaaa ATGGCGAATT GTATCAGAG AAATGCTCTT TTCTCTCTGA  
           541 CTCTCTCTTT TTTATTGTCA GTCCTCAAC TCGTTCAGgt aaacactca aaacagattc  
 15          601 agtttattaa agtctgatat tgaagtittta tatattacag gctgtctcgt gaggtaaaaa  
           661 tgaccaaaag ctatacatte cttaaaaatt taatggctat tagttttctg atattgaagt  
           721 ttatatataa tatgacagcc TCGTGGTGGT GGTGGCAAC TCANACCCCA AGgtacggac  
           781 tcaaaatttt tgttgtttca tatgactata ttastttatt aatcactaat tatgtataat  
           841 gttgataaal aaacttttaa gtacacaaan tgggtttatt ttgtgaaat gtccgttttc  
 20          901 tagtataactg tatgtgtgta attataagca tgaacataaa gatctcaatg atttgtttt  
           961 tgtttgtttg ttgtgatag ctctttttgat ggaacactca attgttagt GCAACTCAAA  
           1021 GTGTAGCTTC CGTTGTTGAG CAACATCACA CAAGNAGCCA TGCAATGTCT TTTGCTCAAA  
           1081 GGTGTCAAAA AAATGCTCTT GTGTCTCTCC TGGCACTTTC GGCAACAAAC AAATGTCTCC  
 25          1141 ATGTATCAAC AACTGGAAGA CTAAAGAGG CGGTCAAAA TGTCCTTAAa actctttttt  
           1201 agatatattt gataatatuc abtagatttt ggaattatca aacttactca ctctgtttta  
           1261 atctgtttct acaagttggc gattttgtct tacacttttt ttgtgtcttt tgctcttaac  
           1321 tgttgtgttt gttatacgtg taagcccgcc caatgtgtca tggccgaact tatattaggt  
           1381 acatatttat gaaatgggct tcaattatcaa ttgatttgag cctacaaaaa tgaagccata  
 30          1441 aagoccatia agttgtaatt gttaatattt cagtcataaa tatgattttc tatatctatg  
           1501 atttatotct agtgttgatg atgtttgatg gtgggaagta tgttctattt gcttccacgg  
           1561 tttaaaacc atcaactgyc taaggtaaa ttcataatt actgtgaaa acatattia  
           1621 cgtgcgtaat tatatgaatt tatgaatagg tttaaattcc atttttscat aatagtttt  
           1681 tatgtcaaa (SEQ ID NO: 17)

35

MANCIRENALFFLTLFLLSVSNLVQAA

40 RGGGKLPQQ

CNSKCSFRCSATSHKKPCMFCLKCKKCLCVPPGTFGNKQTCPCYNWWTKEGRPKCP\* (SEQ ID NO: 18)

45

I. At4g09600 (GASA3)

1 taggctggca atttaactct gagaactctt tcttgtatag agaataaac atacgcggtgt  
 5 61 aaagaaaaac gcgtgaactg aatgatgagt gttaacgttc gctcgagatg ccaccaaaac  
 121 ttttcattaa atgtgaattgt ggaaggacat ccacttttaa cgaagtcatc tccactgggt  
 181 gacatgtgga ctctactttg ggtggcatgt tcatatcttt ccacatcacc atgtaaacgt  
 241 gaaaacaccc accacactca cttaactctc aaacacatgt cttcattatc gtacgtagct  
 301 ccaaaaaaaa aatgaaaaac taggtttagt gattctattt cgaatgtat aatatacaac  
 10 361 ttgtaaaaat aaatattttg aataagcatt ataataaac ccaagaggtt gttagattta  
 421 tatacttaac tgtagtactt aaatagagaa tcagagagaa tagttttata tcttgcacga  
 481 aaatgcalgc ttittgagac tggcgaattc tccgaagcac actaatgttta ctctgatacc  
 541 TCTTCTGCTT CACCACCTTT GAGgttcaata acttttgtct ttaactctcc atgaatcatt  
 601 tgcttcgtct tatccttaac tcatatgtgt ttgatcaatg ataataatc atcattctct  
 15 661 tcaagCTTCA GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGCGGTAG TGAJAATTGg  
 721 tatgtaacgc taacatatat gtaagtggtt atatctctgt ttatatatga tttttaaacg  
 781 gtttaaaact agtcatatgt gtaataatat atcatgtgaa gATTGCGGTG GGAGATGCAa  
 841 AGGTGATGTC AGCAATGCTT CAGGGCAAA TCTGTGTTTG AGACATGCA ACAGCTGTGg  
 901 TTACCGCTGC ACTGTGTGTC CACCAGGCAC CACCGGGAAC CACCACCTTT GTCTTCTTA  
 20 961 CGCCTCCATT ACCATCTGTC GTGGCGCTCT CAAGTCCCTT TAAacataata caactacaga  
 1021 tgttgtgata tgtcttcgcg gacacacacg gtactgttat gttttaagga caatagtatg  
 1081 tatgagcagc tataaacaaa ccagaagtta atggttcagt ttgaactagt ataagttgta  
 1141 tgaactgtgc ttcttttgea caaccacttt tgcgtgaagt ttagcaaccc tatttaataa  
 1201 attagagatt ccaaaaaaaa aaatgaaaaa tgtttaaaaa acygtggatt tttaatttgg  
 25 1261 gattaaaaat taattttcat ttgtgttagt tgtcaataaa attagctaaag ttttgtatc  
 1321 taggcggttt aagatatgct gttaaatttt tgataataga gtgacttag aagttcaata  
 1381 ctgtaaatat ctaactcac ttcaattctca caaacacag aatcaacttc agactaaga  
 1441 atcgaaatga ccagaactga aagaagtaa aagaaaagct gaatacagag aatttaacga (SEQ ID NO: 19)

30 MAIFRSTLVILLILFLTF  
 ELHVHAAEDSQVGEVVKID

35 CGGRCKGRCSKSRPNCLELRACNSCCYRCNCVFPGTAGNHHLCPYASITTRGGRLKCP\* (SEQ ID NO: 20)

J. At4g09610 (GASA2)

5           1   ttaacagttt   aacaccataa   tgttaaacctc   gytttagcat   tttggtgtaa   ttctacctct  
           51   ttaaccatac   atcactaaga   cgcagagaag   ttcatatggg   agttaatcgt   aaatagctaa  
           121   acttttaaat   ggggttaaca   tattatttaa   cactatacat   ttaaactatg   atctctcaat  
           181   ttttttttat   taaccaaaat   aaattcattt   tagaaccaaa   cgtttcaaaa   actcgttaag  
           241   ttttctcaat   aaatcttatac   tatagctcac   acaagaataa   actcagacac   tgactgcacc  
 10          301   caattatata   catggtattat   tatttttagt   gttataatat   gatacaaaat   aaaaaacatt  
           361   tgagtagccg   ataggcgata   gccactataa   atataccaaa   gaggttggtat   tatacatata  
           421   gcggtaatatc   caaagagagt   atcagataga   atagtctcta   atattttgta   caactcacag  
           481   aaattgcacg   agtttcgaac   ATGCGCATCT   TCGGAAGTAC   ACTGGTGTCT   TACTATAACA  
           541   TCGTCTGTCT   CACCACTTAT   GAGgtttata   atattttggg   tctttatagt   tccocnagaa  
           601   cacctagcaa   tattatactc   aattcatggt   tatatgataa   tgactgatca   ttctcttcag  
 15          661   CTTCACGTCC   ACGCTGCTGA   TGGTGCAAG   GTCGGTGAA   GGTAGTGAA   AATCGgtatg  
           721   taaccctaac   ttatatataa   cacgttggta   tataacttaa   tattctgat   gggtgcactc  
           781   tcttcccaac   ttatatatat   ctttgtttatg   gagaatgtct   caagcttita   atgagatgtt  
           841   atatctcgga   gaaggaaact   atgacataaa   agctttggtat   tcccttgcaa   caaatataaa  
           901   cttttgatgg   gtttaaacgg   attaaattag   ttacatgtgt   ttggtgaatg   tatgtatgat  
 20          961   tgtagaTTGT   GGTGGAGAT   GCNAAGATAG   ATGCAGCAA   TCTTCAGAA   CGAAGCTATG  
           1021   CTTGAGAGCG   TGCACACGCT   GTTGTTCGCG   GTGCAACTGT   GTGCCACCTG   GTACTTCTGG  
           1081   AAACACCCAC   CTTTGTCTCT   GCTACGCTC   CATTAACACT   CACGCTGGCC   GCCTCAAGTG  
           1141   CCCTTAAaat   ttcttctgtg   tcgtttttctg   ttctactctc   tatttogaat   atagtacat  
           1201   gtgtgtgtac   gtgtgtatgt   atacaagtac   tgttatgttt   tggaggacaa   aagtataigt  
 25          1261   atgagaagct   ataaactaat   tagaagtgtg   tggttatgcy   tattatcaaa   cogytttact  
           1321   tcctgaacaac   caatttcggt   tgtttccaa   tttggcaacc   ctaaaataaa   aattcaaaat  
           1381   gattggagac   tactcgttaa   tagacattga   aaacagtga   atctcgttac   gtttttatat  
           1441   tttttgaaact   gtaatatatt   tatgcagaag   cgyttttgta   atgggcgcac   aaaaaaaaag  
           1501   tggttttgta   atggaatgta   ttcggatcta   ttctggaat   ggtctcaaaa   agttaggttg  
 30          1561   agatctcaat   acgaanaatga   accttttctg   ttgaatttat   aaagcctttt   attttgaaaa  
           1621   cgttaaatcc   tcaactagat   ctctcttt   (SAQ ID NO: 21)

35 MAVERSLVLLIIVCLTTY

ELHVHADGAKVGEVVKID

CGGRCKDRCSKSSRTKLCILRACNSCCSRNCVPPGTSGNTHLCPCYASITTHGGRLLKCP\*\* (SEQ ID NO: 22)

40

**K. At5g15230** (GASA4)

1 aaatattcac cctaaaatga atctaaaaat gtacaaaatc acaggaaaaa aaaactaagc  
 5 61 agaagtgcoc taagaaaaact aaagttttta aaaaataatc ttcaaaagaga tactccaact  
 121 ggtgtttata gcaaaactgt attatcaaa acagagttca tagtttttta tatttagtag  
 181 tataagcttt ccttaaacca tgtgcaaaac catctaccgc agtctaatta ccaatagaaa  
 241 gtaataaaat gggactaaca ttggaggcat acgttggaata atataattgg aggaatacacg  
 301 taataatgat atgtgttgcc acagggaata attgatacga gcaaatgtgt gtatatatag  
 10 361 cttatatgca acatcatggy gtccctcaacc aaaaactcct ctctcagtac actctttttc  
 421 atacctcaag agactaaaaac tagttttgag agatttagag gagtgttttg ttttttggat  
 481 aacataatcc caaactgaia ATGCTTAATG CATTAAGAGC TATCTACCTC TTGACCCCTC  
 541 TTGTCCTCTT CATGCTTCAA ACCATGgtaa cccctctatt attttttct tcttcaaty  
 601 tttgaaaata ttgaagataa takatttgat tgttttctct attgacgaac gatatgagac  
 15 661 aaatgtgggt tctatatatt taacttttagt tggaaatata ttaattttagc ctttttaattg  
 721 aaattaattt taactgtttt tctctctctct ttttttgggt ttttagGTTA TGGCCTCAGG  
 781 TGGATCTAAT GTGAAGTGGG GCCAGgtcag tttttatttt gaatcgacta gtaattacct  
 841 tttaaaactat atttttatcc tttgtttatc tctgaactta acgaagaatg attaatagt  
 901 taactttttt gtttaatttt cagaaACGTT ATGGACAGG AAGCCTGAAA COTACCCgtt  
 20 961 agttttttct tcacagctat tcttaaacaa ttttttttta atctcataat cgcaggaana  
 1021 taacaacttc aagaaactct tttattgttt ataataaaaa aaaaataagca ttctcagtgc  
 1081 agaaaaaagc ttgaagatga agtgttaagt ggaactgttg gtacagatccg tagactcaaa  
 1141 atatatatga tattgacgaa attgcccctt aatatgttca tacagtcaaa gcaaccact  
 1201 atcttgagac ccaaaaaacs gtaaaaaaaa aagctaatga atttccacta gattctgttg  
 1261 tttttatag taataaaaaa tttttgagtg ttaacttttt gatatttttt gttattgaaa  
 25 1321 caaccagAAT GCCATCGA ATGTGTAGG AGGTGTAAA AGACACAGTA CCAACAGGCT  
 1381 TGCATTACGT TCTGCACAA ATGCTGCAGG AAGTGTCTCT GTGTGCCTCC GGGTACTAT  
 1441 GGGACAAAC AAGTTTGCTC CTGCTACAAc AACTGMAAA CTCAGAGGG TGGACAAAA  
 1501 TGCCCTTGaa aaastctccc ttoyttccct ttttaataa aaaattttca actataacta  
 30 1561 aatttccott gatcaatgtt ttactacttt tattctaat gttgtaagt tatgtcaact  
 1621 cttttcgggt ttgtcttaa abctaaaaa aaatgagatg ggcctatga atgatattt  
 1681 tcatgaaatc ttgtgttct aaagatattt toccattcat ccaccaaaaa aaagatatt  
 1741 ttccatttgc aaatatgtaa tactataaag ggtangcaaa acaataaat acaatttaa  
 35 1801 aaattcctgc gaagaagta tgcatatgta gaaaagagt acattgggtc tctcgcocaa  
 1861 gtactaaaaa gccattattt gatttttcaa agctttttac aaatcactg gtctaacgr  
 1921 gatgtcttt tgcgcgaatc ttcttttata caagactgg gctttgggca gttggaata  
 1981 aataacyaca acyatatttt acaatcgtt (SEQ ID NO: 23)

MAKSYGAIFLLTLIVLFLQTMV

MASSGSNVKSQKRYGPGSLKRTQ

CPSECRRCKKTYQHACITFNCKCRKCLVPPGYGNKQVCSYNWRTQEGGPKCF\*\* (SEQ ID NO: 24)

L. At5g14920

1 ttgtctcactg gtgcaataat cgaagtgaa agcctcttta tatgaataat ataagcgaca  
 5 61 cagccttatg ggcgaatcga atgctattta ttattttgat aagaagatta ataatttcoa  
 121 ttgtgtcaacc actagtctct ttgggtacttc aaacatatc accaaaagt ccatagagtt  
 181 atttgtctct attactatg aaggtatctc aagtgatgt acgaataag tggcaatttc  
 241 atgtattatc atataatacc atttttggga atctgatatt ttgtttatcc tcagagctctg  
 301 agagatatat tttygtgcag tgaaggttca aagctgcat gcatgatgca tacaataat  
 10 361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat attgttaata  
 421 aataaggaa tcctatttat atcacaaaag gtcaactggtc ttcttcgtgt gacttoaaca  
 481 ctttctcaac tccacaasaa ATGGCTCTGT CACTTCTTTC AGTCTTATTC TTTTTCATG  
 541 TCTTTACCA Ttaagtttat tcttacttt catataasaa pgtgttaata tgttaagpac  
 601 tacataatag tatacaatta ttgtcattac gtitttcggt attgttaacta actatgtatt  
 15 661 ttgattaatc accgacagag TTGTTTTCG TGCTTCAAA GAGGAATCCA ACSCCTTAgT  
 721 acgttttcta atttcaggt taattatttc tatgctctt taactatata ctcaagcatt  
 781 tttattgatt atttgtgatg aagtttaatt ttggtatatg ttgtattaa atttatagGT  
 841 TCTTTACCA ACGCAACAC TTCCATGCGC ATCTCGGGT ACCAACCGC CGTGGCGAGC  
 901 TCCAAJAGCG CCGAGCGCG GTTACAGCC ACCAGCGCT CCAGTACTC CTATTAAACC  
 20 961 ACCCAACCA AAGCGTCGG TCANACCTCC ANGTATGCG GTTACCGG TAAJACCTCC  
 1021 GGTTTCAACT CTCGCGATCA AACTACCGCG GGTACAACCA CTAAGTACA AACCGCCAC  
 1081 GCCAACAGTT AAACACCGCT CCGTCCAGCC ACTACGTAC AAACCCCA CTTCAACGGT  
 1141 TAAACACCGC ACTACATCAC CGGTTAAACC ACCACTACG CCACAGTTC AATCAACGGC  
 25 1201 GTTCCAAACA CTAAGTACA AACCGCCAGC GTCACGGT AAACCCCA CCAACAGTCC  
 1261 ACCGTTTAAA CCGCCACCA CAGCGCACCC GTCCACACA CTAAGTACA ATCCCGCAC  
 1321 TACACCGGTT AAACACCTA CAGCGCGCG TTGCAAACT TGTCAAACT CTCGCGTAG  
 1381 AACTCGGATA Ggtaataata attttcttc aaagtgtag tgattatcg tcgttgata  
 1441 gatcgatgt ataatggac taatttttg acggttaga TTGCGTCCCT TTATGTGGGA  
 30 1501 CGAGGTGTGG GCNACCTCG AGGAAGTAG TATGTATGAG AGCGTGGTCC ACCTGTGCT  
 1561 ACCGCTGCAA GTGTGTTCC CAGGCGACT ACGTATATA GGAGAAGTGT GGATCTGTT  
 1621 ACCGCAACAT GAGACAGCT GTTGGAAAT CCAATATCC TTGAACATT tatatagat  
 1681 ggtgttaaa cgaataatt taactcaat gagtittat aagtttgaa tgcgtttgt  
 1741 ttgttatag taatttgag ttggtcttt gttaacggga cgtagaatc taataatga  
 35 1801 aaaaaacctc ctgcagaa taagggttt atgaattgt ttgtattga ataataag  
 1861 gatggataaa gtttattat tctaacaggt tactttatta ggcatttctt cgcctcaat  
 1921 aactcttgta tgcgtgaac tatgtaag atagaagaac ctasaaaag aagaasaca  
 1981 agaatgac atagcgaac tcaaaagat agttgtctgc tagcgttaat ttgttattc  
 2041 agttgggca atagctcaa tgcgaactc taattggcc tatataag cttatgtgc  
 40 2101 atatggtcaa gctatttgg gccatgtgt ttgaagatca ttgggaag tcttgcgcaa  
 2161 ggaag (SEQ ID NO: 25)

MAISLISVFII FHVFTNVVFAAS

45 NEESNALVSLPTPLPSPSPA  
 TKPPSPALKPPTPSYKPTLP  
 TTPKPTTKPFVKPPTTFT  
 FVKPFVSTPKLPLFPVQPTT  
 KPPTPVKPPSVQPTTKPPT  
 50 PTVKPTTSFVKPPTTPPVQS  
 PFVQPTTKPPTSFVKPPTT  
 PFVKPPTTFPVQPTTNPPT  
 TTVKPTTAPFVKPPTFPVPT  
 RID  
 55 CVPFCGTRCQHSRGNVCMRACVTCYRCCKVPPGTGYNKKKCGSCYANKMTRGGKSKCP\* (SEQ ID NO: 26)



**M. At5g59845**

5           1   gac ttg agt a   tga stccaat   aacc ccaaat   ttag tgcagat   tttagaat ac   ttcttataaa  
           61   tcttasa tga   ataccaaa   actttaacet   acttttaaca   aatcttgatt   gaataacac  
           121   agattctaca   tgcatttta   antcactaaa   actcttttga   aatcnaaac   caataacacg  
           181   cccttagttt   tttactattt   gaattctgac   gtactttttt   attagttgaa   ttctataaa  
           241   tgagaaaaca   ttaattattt   cttaactctt   gaacttaagc   ccccaaaaa   tcttataat  
 10        301   tgggacagat   ggactagata   acaagcgttt   cacttaactc   aaaatttccc   tataagtaac  
           361   tcttttttga   acctctcttt   cttcccaaac   catcactctc   tttgattgt   gtgaaacctt  
           421   cgagttttct   cttccctctc   tcaagtaaac   aaactttctc   caaacagatt   atttataaaa  
           481   caactctctc   aagaactacg   ATCAAAATCC   CGGCTGTAAA   AGTTCATTAT   ATCTCTCTTC  
           541   TCATCACATC   TTCTTTGTTC   ATACTCTCAA   CCGGGGATTC   GTglaagtal   acacaa tga  
           601   ttttcttatt   ttagatactt   ttctcattag   aaatttagct   ttcttaataa   aattgtattg  
 15        661   tga tga tgg a   ttaattagCA   CCATGCCGAG   GAAAATGCAA   CGTGAGATGT   TCAAAGGCAG  
           721   GAAGACAAGA   TAGGTGTCTC   AAGTATTGTA   ATATATGTGTG   CGAGAAGTGT   AACTATTGTG  
           781   TTCTTTCAGG   CACTTATGGA   AACAAAGATG   AATGCCCTTG   TTACCGCGAT   ATGAAGAATC  
           841   CCAAAGGCAC   GTCCAAATGT   CCTTGACat   gttcttaaga   ttatccttat   agacacaata  
           901   tcttgaatgt   tlaagattgt   gcttgatgcc   taaaataatg   agcttgagat   acttctatga  
 20        961   atgaatatgt   gaaagatttt   gacaaataaa   tgatttgatg   tattaaata   ttcttagtga  
           1021   agttatatat   gtataaatga   agtatgaat   atacattgta   tgttgcttta   catgagaag  
           1081   ataaatctac   aacaatccaa   tgtatgaaa   tillactaag   ttaactgata   agaaacgtta  
           1141   attatggttt   agaatcttgt   ggagagatga   ttacttttgt   aagsgaatt   gattgttgt  
           1201   tgtcaatgag   gataagtas   gaagcaattt   ctcaacacat   ggacttgata   gcaaacataa  
 25        1261   caagcctcaa   gcattgaaat   tgaacgtct   cgtatagtaa   gatttgctca   agaaagcaa  
           1321   gtgttttttg   tttagaanaa   cagaatattga   aattactgtc   tactttt

(SEQ ID NO: 27)

30 MKFPVAVKVLIISSLITSSLFILSTA

DSSP

CGGKCNVRCSKAGRQDRCLKYCNICCEKNCYCVPSGTYGNDECPYCRDMKNSKGTSKCF\* (SEQ ID NO: 28)

35

**N. At3g10170**

genomic structure before splicing and processing 5' - towards 3'  
 predicted orf sequences are underlined

5  
 10  
 15  
 20

CTGTTTTCAGAAAATGGCAACAAAAGTTAGCATCATTTGTTTCTCCATTG  
TGAGTTACATCTTCTTCTGTCGTGCCCATATGCATGTAAGTGTTCACAC  
CTCTATCTCTTATGTTACATTTATCAACTTTATCTATACGTCCTGTA  
ATAAAACACAGCCTATATACTTGGATCTCCTGCTCGAACACACAAACA  
CCACAGTCGCACACCAACTGCCGATCACAATACTCTACAGTGAGTTT  
CTCGGTTCACTACTACTCAAAAAAAGAGTTTCACTCGAATCTACAAAACCT  
TTTTAACATCCTTTGCATCTTCTTGTGATTTTGGCACTACGGTAACACT  
CAGGCGAGTCTTCMACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA  
ATTATGTTTGTGCTGAATGCGAAACTAATCCGCTATTCACACTTTATT  
AGAGTCGGGCGCAAGGTGTGGATAGATGCTCGAATCAACAATACAGA  
AGCCGTGTTTGTCTTCTGCAACAATGTTGTACAAAGTCTTGTGTCTG  
CCCCAGGTACTTATGGCAATAGCAAGTATGCTCTTATCAACTG  
AGAGACCAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA  
CTTTAGCATAACTCCATGTAATTTGTTAATCTACCTATCATATAATTATA  
TATGTATTGGACTCTTCCATAATCMATCAGTTCTCTGTATTATGACGT (SEQ ID NO: 29)

Amino acid sequence of the predicted pre-pro-peptide  
 the first line represents the signal sequence  
 the second (set of) lines represents the the pro-peptide  
 the last line represents the conserved Cysteine motif.

**MATKLSIIIVFSIVVLHLLSARMH**

**FLINVCAECETKSAIPPLLE**

**CGPRCGDRCSNTQYKKPCLPFFCNKCCNKCLCVPPGTYGNQKVCPCYNWTKSGGPKCP\*** (SEQ ID NO: 30)

35

- They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cystein residues. The Consensus of this last domain is:
- C-C-RC-----C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP\* (SEQ ID NO: 31)
- (-) = any amino acid;  
(C) = conserved C-residue  
(/) = either one or the other amino acid at this position;  
\* = stopcodon

- Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis* *thaliana* (Plant Mol. Biol. 36 (1998). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different membres, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).
- Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL  
5 proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression  
10 cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in arabidopsis and in rice:

Gene code	contig	gene prediction in At database	Oryza sativa japonica contig	approximate position in bp around:
5				
RKS0 At1g71830 f14c23	ok		OSJNBa0036B21	52.000
RKS1 At1g60800 f8a5	ok		P0038C05	60.000
RKS2 At5g65240 mqn23	ok		QJ1212_C08	8000
RKS3 At5g63710 mbt5	ok		see rks2	
10				
RKS4 At2g23950 t29e15	wrong, exon missing		P0708B04	35.000
RKS5 At5g45780 mra19	wrong, exon missing		QJ1077_A12	102.000
RKS6 At5g10290 wt e 23	ok		see rks2	
RKS7 At5g16000 ku e 24	ok		P0038C05	60.000
15				
RKS8 At1g34210 f23m19	ok		QJ1134_B10	90.000 & 1000 2
different genes!				
RKS10 At4g33430 en d 25	wrong, exon missing		see rks0	
RKS11 At4g30520 wu d 20	wrong, exon missing		see rks4	
RKS12 At2g13800 fl3j11	wrong, exon missing		see rks10	
RKS13 At2g13790 fl3j11	ok		P0633E08	36.000
20				
RKS14 At3g23560 mw12	wrong, exon missing		OSJNBa0015G09	36.000
ELS1 At5g21090 ch e 52	ok		P0003H10	53.000
ELS2 possibly allelic variant of ELS1 no genomic sequence identified yet	ok		see els1	
ELS3 At3g43740 by c 21	ok		P0468B07	52.000

Homology between aa sequences from arabidopsis proteins are compared with the rice databases using:  
[http://mips.gsf.de/prot/hal/db/search/search\\_frame.html](http://mips.gsf.de/prot/hal/db/search/search_frame.html)

protein sequences based on *Oryza sativa* japonica contig sequences.

*Arabidopsis thaliana* ELS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```

ttactctcaaattccttttcgattccctctctttaacctcgaaagtcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGAGCTTCGTTAACCTAA
CCTTAGCTTTGATTCACTGGTTCGAAGCAAACTTCGAAGGAGATGCTCTTA
CGCTCTTCGCGGAGTTTGACAGATCCAGACCATGTCTCCAGAGCTGGGAT
CCAACCTCTGTTAATCCTTGTACCTGGTTCCATGTACCTGTAAACCAAGACA
ACCGGCTCACTCGTGTGGATTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCTTGAGCTTGGGAGCTTGAACATTACAGTATCTAGAGCTCTACAAAAAC
AACATCCAAGGAACATATACCTTCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAAACAATCTTACAGGGATAGTTCCTACTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGCTC
AAGCAATGATTGTGTGGACAATCCCAAAACGGACCTTTGCTCACATTCC
TTTACGAACCTTTGAGAACAACCGAGATTGGAGGGACCGGAATTACTCGGT
CTTGCAAGCTACGACATAACTGCACCTGaacaaactggcaaaacctgaaaat
gaagaattggggggtgaccttgaagaacacttcaccactttatcaaatatc
acatctactatgtataagtatatatgtagtccaaaaaataaaaaa (SEQ ID NO: 32)

```

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL  
TLTLALIHLEVEANSEG

10

DRLYALRRSLTDF  
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA

15

P ELGKLEHLQYLELYKNNIQGTI  
PSELGNLKNLISLDLYNNNLTGIV  
PTSLGKLKSLVFLRLNDNRLTGPI  
PRALTAIPSLKVVDVSSNDLCGTI  
PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT (SEQ ID NO: 33)

*Arabidopsis thaliana* ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 aaaattactcaaatcctattagattactctcttcgacctccgtagctcac  
ATGGCGCTCGAAACTATCGGTGGGAGCTCTTCGAGCTTCGTTAATCCTAA  
CCTTAGCTTTGATTCACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTTTA  
CGCTCTTCGCCGGAGTTTAAACAGATCGGACCATGTCTCCAGAGCTGGGAT  
CCAACCTCTTGTTAATCCTGTACCTGGTTCATGTCACCTGTAACCAAGACA  
15 ACCGCGTCACTCGTGTGGATTGGGGAAATCAAACTCTCTGGACATCTTGC  
GCCTGAGCTTGGGAAGCTTGAACATTACAGTATCTAGAGCTCTCAAAAAAC  
AACAATCAAGGAACTATACCTCCGAACCTGGAAATCTGAAGAATCTCATCA  
GCTTGGATCTGTACAAACAATCTTACAGGGATAGTCCCACTTCTTTGGG  
AAAATTGAAGTCTCTGGTCTTTTACGGCTTAATGACAACCGATTGACGGGG  
20 CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAAGTTTGGATGTC  
TAAGCAATGATTGTGTGGAACAATCCCAACAAACGGACCTTTGCTCAGAT  
TCCTTTACAGAAGCTTTGAGAACAACCCGAGGTTGGAGGGACCGGAATTACTC  
GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaattggcaaaacctga  
aaatgaagaattgggggggaccttgtaagaacacttcaccactttatcaaat  
25 atcacatctactatgtaataagtatatatgtagtccaaaaaaaatgaa  
gaatcgaaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt  
atgaaaattaaagattgtactgtaatgttcggttggtgggattctgagaagta  
acatttgattggtatggtatcaagttgtctgcctgtgtctgcaaaaaaaa (SEQ ID NO: 34)

- 30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

- 35 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain



contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be  
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL  
ILTLALIHLEVEANSEG

10

DALYALRRSLTDP  
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSCHLA  
P ELGKLEHLQYLQLYKNNIQGTI  
PSELGNLKNLISLDLYNNNLTGIV  
PTSLGKLKSLVFLRLNDNRLTGPI  
20 PRALTAIPSLKVVDVSSNDLCGTI  
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT (SEQ ID NO: 35)

25

*Arabidopsis thaliana* ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctctccggcgaaasacc**ATGGTGGGCGCAAAACAGT**CGGCGGGAGCTTCTAGCAGCTT  
CCCTGATCCTAACTTTAGCTCTAATTGGTCTAACGGAAGCAAACCTCGAAGGGGACGCTC  
TTCACGCGCTTCGCCGAGCTTATCAGATCCAGACAATGTTGTTCAAGSTTGGGATCCAA  
CTCTTGTTAATCCTTGTAAGTTGTTTCAATGTAATCAACACCATCAAGTCACTC  
GTCTGGATTGGGGAAATCAAACCTTATCTGGACATCTAGTACCTGAACCTGGGAAGCTTG  
15 AACATTTACAATATCTTGAACCTACAAAAACGAGATTCAAGGAACCTATACCTTCTGAGC  
TTGGAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACAACAATCTCACCGGGAAAA  
TCCCATCTTCTTTGGGAAAAATTGAAGCGGCTTAACGAAAACCGATTGACCGGTCCATTTC  
GTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAAATGATTTGT  
GTGGAACAATCCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAACTTTGAGAACA  
20 ACCTGAGATTGGAGGGACCAGAACTACTAGTCTTCGCGAGCTATGACACCAATTGCACCT  
AAaagaagtgaagaa (SEQ ID NO:36)

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

- 25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).
- At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
- 30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each
- 35 approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL  
ILTLALIRLTEANSEG

DALHALRRSLSDP  
5 DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV  
10 P ELGKLEHLQYLELYKNEIQGTI  
PSELGNLKSLSLDLYNNNLTGKI  
P SSLGKLKRLNENRLTGFI  
PRELTVISSLKVVDSGNDLCGTI  
PVEGPFEPHMQNFENNRLLEGPE

15 LLGLASYDTNCT (SEQ ID NO: 37)

*Arabidopsis thaliana* RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 attttttatttttttttactctttgtttgttttaatgctaagggttttttaaagggtt  
atcgaaaaaatgagtgagtttgtgtgaggtgtctctgtaaagtgttaagggtggtgat  
tttcggaagttagggttttctcggtatctgaagagatcaaatacgaattcgaaatttacc  
ttgttgtttgaaATGGAGTCGAGTTATGTGGTGTTTATCTTACTTTCAGTGATCTTACT  
CGAATCATCTACTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTGCATACTTTG  
15 AGGGTTACTCTAGTTGATCCAAACAATGCTTGCAGAGCTGGGATCCTACGCTAGTGAAT  
CCTTGCACATGGTTCATGTCTACTTGCAACAACGAGAACAGTGTCTAAGAGTTGATTTG  
GGGAATGCAGAGTTATCTGGCCATTAGTTCCAGAGCTTGGTGTGCTCAAGAAATTGCAG  
TATTTGGAGCTTTACAGTAACAACATAAATGGCCCGATTCCTAGTAATCTTGGAAATCTG  
ACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGCTCTATTCCGGAATCA  
20 TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGCTTAAACAACAAGCTCTACTGGGTCA  
ATTCTTATGTCACTGACCAATATTACTACCTTCAAGTGTAGATCTATCAATAACAGA  
CTCTCTGGTTCAGTTCTGACAAATGGCTCCTTCTCACTCTCACACCCATCAGTTTGTCT  
ATAAATTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCTCTGGATCTCCCCGTTT  
TCTCCTCCACCACCTTTTATTCAACTCCCCAGTTTCCACCCGAGTGGGTATGGTATA  
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCTGCA  
ATAGCCTTTGCTTTGGTGGCGACGAAGAAGCCCACTAGATATTTCTTCGATGTCCTGCC  
GAGAAGATCCGAAGTTTCATCTGGGACAGCTCAAGAGGTTTTCTTTGCGGGAGTACAA  
GTGGCGAGTGATGGTTTAGTAACAAGAACATTTTGGCGAGGTGGTTTGGGAAGTC  
TAGAAGGAGCGCTTGGCAGACGGAATCTTGTGCTCAAGAGACTGAAGGAAGAGCGA  
30 ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTAGTGGCAGTTCAT  
CGAATCTGTTGAGATTACGAGGTTCTGTATGACACCGACCGAGAGATTGCTGTGTAT  
CCTTACATGGCCAAATGGAGTGTGCTTCTGTCTCAGAGAGAGGCCACCGTCAACAACCT  
CGCTTGTATGGCCAAACGCGGAAGAATGCGCTAGGCTCAGCTCGAGGTTGTCTTAC  
CTACATGATCACTGCGATCGAAGATCATTCACCGTGACGTAAAAGCAGCAAAATCCTC  
35 TTAGACGAAGAATTGGAAGCGTTGTTGGAGATTTCGGGTTGGCAAAGCTTATGAGCAT  
AAGACACTCAGTGACAAACAGCATCCGTTGGCACCATCGGTACATCGCTCCAGAAATAT  
CTCTCAACCGGAAATCTTCAGAGAAAACCGAGCTTTTCGGATACGGAATCATGCTCTTA  
GAACTAATCAGAGCAAAAGAGCTTTCGATCTCGCTGGGTAGCTAAGCAGCAGACGCTC  
ATGTTACTTGACTGGGTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT  
40 CCAGATCTTCAAACAACTACGAGGAGAGAACTGGAAACAGTGATACAAGTGGCGCTG

CTATGCACGCAAGGATCACCAATGGAAGACCAAGATGCTGAAGTTGTAAGGATGCTG  
GAAGGAGATGGGCTTGGGAGAAATGGGACGAATGGCAAAAGTTGAGATTTGAGGGAA  
GAGATTGATTGAGTCTAATCCTAACTCTGATTGATTCTTGATTCTACTTACAATTG  
CACGCCGTTGAGTTATCTGGTCCAAGGTAAAAA (SEQ ID NO: 38)

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKSO protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MESSYVVFILLSLILPNHSL  
WLASANLEG

DALHTLRVTLVDP  
35 NNVLQSWDPTLVN

PCTWFHVTCNNNSVIRV

DLGNAELSGHLV  
40 P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI  
PESLGKLSKLRFLRLNNSLTGSI  
PMSLTNITTQLVLDLNNRLSGSV  
PDNGSFSLFTPLSFANNLDLCGPV

5 TSHPCPGSPFSPPPP  
FIQPPFVSTPSGYGITG

AIAGGVAAGAAL

10 PFAAPAIAFAWW

RRRKFLDIFFDVPAEEDPE  
VHLGQLKRFSLRELQVAS

15 DGFSNKNILGRGGFGKVKGRLLAD  
GTLVAVKRLKEERTPGGELQFQ  
TEVEMISMAVHRNLLRLRGFCM  
TPTERLLVYPYMANGSVASCLR  
ERPSPQPPLDWFTRKRIALGSA

20 RGLSYLHDHCDPKIHRDVKAA  
NILLDEEFEAUVGDFGLAKLMD  
YKDTHTVTAVRGITIGHIAPEYL  
STGKSSEKTDVFGYGIMLLELI  
TGQRAFDLARLANDDDVMLLDW

25 VKGLLEKKLEMLVDPDLQTNV  
EERELEQVIQVALLCTQGSPME  
RPKMSEVVVRMLE

GDGLAEKWDEWQKVEILREEIDL

30 FNPNSDWILDSTYNLHAVELSGPR (SEQ ID NO: 39)

*Arabidopsis thaliana* RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 ccaagtgtagtgctttaagaagggat**ATGGAAG**GTGTGAGATTGTGGTGTGGAGATTA  
GGATTCTGGTITTTGTATGGTTCTTTGATATCTCTTCGTACACTTTCCTACTGGT  
GTAACTATGAAGTGACAGCTTTGGTGTCTGTGAAGAATGAATTGAATGATCCGTACAAA  
GTTCTTGAGAAATGGGATGTGAATTCAGTTGATCCTTGTAGCTGGAGAAATGGTTCTTGC  
ACTGATGGCTATGTCTCTTCACGTGGATCTTCCTAGCCAAAGCTTGTCTGGTACATTGTCT  
15 CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTGCAAAACAATGCAATCACT  
GGTCCAATTCGGAAACGATTGGGAGGTGGAGAAGCTTCAGTCACTTGATCTTTCGAAC  
AATTCATTACCGGGGAGATACGGGCTCACCTTGGAGAACTCAAGAAGCTTGAATTACTTG  
CGGTTAAACAATAACAGTCTTATAGGAAGCTTGCCTGAGTCTCTATCCAAGATTGAGGGA  
CTGACTTAGTCGACATTTGCTATAACATCTTAGTGGTTCGCTGCCAAAAGTTCTCGCC  
20 AGAACTTCAAGSTAATTGGTAATGCGTTAATCTGTGGCCCAAAGCTGTTTCAAACTGT  
TCTGCTGTTCCCGAGCCTCTCACGCTTCCACAAGATGGTCCAGATGAATCAGGAAGCTCGT  
ACCAATGGCCATCACGTTGCTCTTGCAATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGTT  
TTCTTTACAAGCGGAATGTTCTTTGGTGGAGATATCGCCGTAACAAGCAAAATATTTT  
GAGGITAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATT  
25 AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAAGCTTTCGGAAGAGCGGGA  
TACGGGATTGTGTACAAAGGACACTAAACGATGGAACCTTTGGTGGCTGTCAAAGCTCTC  
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT  
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACGAGGAGAGA  
ATTTAGTCTACCTTACATGCCAAATGGGAGTGTGCGATCACGCTTAAAGATAATATC  
30 CGTGGAGAGCCAGCAATTAGACTGGTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA  
GGACTAGTTTACTACACGAGCAATGTGACCCGAAGATTATACACGCGCATGTGAAGCA  
GCTAACATTCGTTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAG  
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAACTGTTGGCCACATT  
GCACCTGAGTACTTATCCACGGGTCAGTCTCAGAGAAGACTGATGTCTTTGGCTTTGGC  
35 ATACTTCTCCTTGAGCTCATTACTGGTCAGAAGCTCTTGATTTTGGCAGATCCGCACAC  
CAGAAAGGTGTAAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAAACTAAAGCAG  
TTAATAGACAAGATCTAAATGACAAGTTCGATAGAGTAGAAGCTGAAGAAATCGTTCAA  
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACGAAATGTGAGAAGTTATG  
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGAGAAGCGTACTGGT  
40 GAGCATCAGCCACGCCATTGCGACCGGGATGGTAGTCTTTCGCCGCTGTGAGGTAT

TACTCGGATTATATTACAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT  
CGATGA<sup>1</sup>tattgactcactgtttttaaaaaa (SEQ ID NO: 40)

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.
- Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
- 20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVRFVVWRLGFL  
VFVWFFDISSATLSPTGVNYEV

TALVAVKNELNDP  
35 YKVLNWDVNSVD

PCSWRMVSCTDGYVSSL



DLEFSQSLSGT  
LSFRIGNLTYLQSVLQNNAITGPI  
PETIGRLEKLQSLDLSNNSFTGEI  
PASLGELKNLNYLRNNSNLIGTC  
5 PESLSKIEGLTLVDISYNNLSGSL  
PKVSARTFK VIGNALICGPK  
  
AVSNCSAVPEPLTL  
PQDGPDESGETRNG  
10 HHVALAFAASFS  
AAFFVFFTSGMFLWW  
  
RYRRNKQIFFDVNEQYDPE  
15 VSLGHLKRYTFKELRSAT  
  
NHFN SKNILGFGGYGIVYKGHLND  
GTLVAVKRLKDCNIAGGEVQFQ  
TEVETISLALHRNLLRLRGFCS  
20 SNQERILVYPYPNGSVASRLK  
DNIRGEPALOWSRKKIAGVTA  
RGLVYLHEQCDFKIIHRDVKAA  
NILLDEDFAVVGDFGLAKLLD  
HRDSHVTTAVRGTVGHIAPEYL  
25 STGQSSEKTDVFGFGILLLELI  
TGQKALDFGRSAHQKGVMLDW  
VKKLHQEGKLKQLIDKDLNDF  
DRVELEEIVQVALLCTQFNPSH  
RPRMSEVMKMLE  
30 GDGLAERWEATQNGTGEHQPPPLPGMVSS  
  
PRVRYSDYIQESSLVVEAIELSGPR (SEQ ID NO: 41)  
35

*Arabidopsis thaliana* RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.
- Italics indicate the presence of an alternatively spliced gene product.
- 10 tcaattttgtagctcttagaaaaATGGCTCTGCTATTATCACTGCCTAGTTTTAGT  
AGTTTATGGTCATCTGTGCACCAGATGCTCAAGGGGATGCATTATTGCGTTGAGGAGC  
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAAACCAAGTCAAGTCAGCTCTGT  
ACTTGGTCTCAAGTATTGTGTGATGACAGAAGAACATGTTACTTCTGTAACCTTGTCTTAC  
15 ATGAACCTTCTCCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAACCTCAAGACT  
CTTACATTGAAGGGAATGGAATAATGGTGGAAATACCAGAATCCATTGGAATCTGTCT  
AGCTTGACCAGCTTAGATTGGAGGATAATCACTTAACGTATCGCATTCCATCCACTCTC  
GGTAATCTCAAGAATCTACAGTCTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT  
ATCCCGGATTCACTTACAGCTCTATCAAACTGATAAATATTCTGCTCGACTCAATAAT  
20 CTCAGTGGTGAGATTTCCTCAGAGTTATTCAAAATCCAAAATACAATTCACAGCAAC  
AACTTGAGCTGTGTGGCACCTTCCCGCAACCTTGTGTAACCGAGTCCAGTCTCTCAGGT  
GATTCAGCAGTAGAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT  
CTACTAGGATTCTTCTCTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC  
GATTTTGTGGATGTTGCAGGAACGAACTTAAAAAGGTTTGATTTCAGGTGAAGTGGAC  
25 AGAAGGATTGCTTTTGACAGTTGAGAAGATTGCTAGGAGAGGCTTCAGTTGGCTACA  
GATGAGTTCAGTGAAGAATGTTCTCGGACAAGGAGGCTTTGGGAAGTTTACAAGGA  
TTGCTTTCGGATGGCAACAAAGTCGCTGTAAGAAGATTGACTGATTTGAACGTCCAGGA  
CGAGATGAAGCTTCCAGAGAGAAGTTGAGATGATAAGTGAGCTGTTTCATAGGAATCTG  
TCTCGCCTTATCGGCTTTTGTACAACAACAACTGAACGACTTTTGGTGATCCTTTCATG  
30 CAGAATCTAAGTGTTCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTCTCGGAT  
TGGTTCAGGAGGAACAGATTGCGTTAGGTGCAGCAGGAGACTCGAATATCTTCATGAA  
GACTTGCAACCCGAAGTCATACACAGAGATGTGAAGCTGCAAGTGTGTACTAGATGAA  
GACTTTGAAGCAGTGGTTGGTGATTTGGTTTAGCCAAAGTTGGTAGATGTTAGAAGGACT  
AATGTAACCACTCAGTCCGAGGAACAATGGGTATATTGCACCAGGAATGTATATCCACA  
35 GGGAAATCGTCAGAGAAAACGATGTTTTCGGGTACGGAATTATGCTTCTGAGCTTGTA  
ACTGGACAAAGAGCAATTGATTCTCGCGGTTAGAGGAAGAAGATGATGCTTATTGCTGA  
GACCATGTGAAGAACTGGAPAGAGAGAGATTAGAAGCATAGTAGATAAGAAGCTT  
GATGAGGATTATATAAAGGAAGAAGTTGAATGATGATACAGTAGCTCTGCTATGCACA  
CAAGCAGCACCGGAAGAACGACCGATGTGCGAAGTAGTAAGAATGCTAGAGAGAGAA  
40 GGGCTGCAGAGAGATGGGAAGATGGCAGAATCTTGAAGTGACGAGACAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTGTGATTGGGGTGAAGATTCCATTAATAATCAAGATGCTATT  
GAATTATCTGGTGGAGATAGaaacaaaaaa (SEQ ID NO: 42)

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.
- Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
- 20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
- 30 product.

MALLIITLVFSSL  
WSSVSPDAQG

- 35 DALFALRSSLR  
ASPEQLSDWNQNVQD

PCTWSQVICDDKKHVTSV

T L S Y M N F S S   G T L S S G I  
G    I L T T L K T L T L K G N G I M G G I  
P E S I G N L S S L T S L D L E D N H L T D R I  
5   P S T L G N L K N L Q F L T L S R N N L N G S I  
P D S L T G L S K L I N I L L D S N N L S G E I  
P Q S L F K I P K Y N   F T A N N L S C G G  
  
T F P Q P C V T E S S P S G D S S R K T G  
10   I I A G V V S G I A V I L  
L G F F F F F C  
  
K D K H K G Y K R D V F V D V A G T N F K K G L I S G E  
15   V D R R I A P G Q L R R F A W R E L Q L A T  
  
D E F S E K N V L G Q G G F G K V Y K G L L S D  
G T K V A V K R L T D F E R P G G D E A F Q  
R E V E M I S V A V H R N L L R L I G F C T  
20   T Q T E R L L V Y P F M Q N L S V A Y C L R  
E I K P G D P V L D W F R R K Q I A L G A A  
R G L E Y L H E H C N F K I I H R D V K A A  
N V L L D E D F E A V V G D F G L A K L V D  
V R R T N V T T Q V R G T M G H I A P E C I  
25   S T G K S S E K T D V F G Y G I M L L E L V  
T G Q R A I D F S R L E E E D D V L L L D H  
V K K L E R E K R L E D I V D K K L D E D Y  
I K E E V E M M I Q V A L L C T Q A A P E E  
R F A M S E V V R M L E  
30   G E G L A E R W E E W Q N L E V T R Q E E F Q  
  
R L Q R R F D W G E D S I N N Q D A I E L S G G R (SEQ ID NO: 43)  
35

*Arabidopsis thaliana* RK33 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aaacgtgtgaaagtgttccatgatcctcttcgaggattcattcaagaaattgctttagatg  
10 aacaatcagaaattgatcttacaatgtttcATGSCCTTAGCTTTTGTGGGAATCACTTCG  
TCAACAACTCAACCAGATATCGAAGGAGGAGCTCTGTTGCAGCTCAGAGATTGCGTTAAT  
GATTTCGAGCAATCGTCTAAAATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT  
TATGTTACCTGCAGAGGCCAGAGTGTGTGGCTCTAAATCTTGCCCTCAGTGGATTACACA  
GGAACTACTCTCCAGCTATTACAAAACCTGAAGTTCCTGGTTACCTTAGAGTTACAGAAC  
15 AATAGTTTATCTGCTGCTTACCAGATTCTCTGGGAACATGGTTAATCTACAGACTTTA  
AACTATCAGTGAATAGTTTCAGCGGATCGATACCAGCGAGCTGGAGTCACTCTCGAAT  
CTAAGACCACTGGATCTCTCATCCAATAATTTAAACAGGAAGCATCCCAACACAATTTCTTC  
TCAATCCCAACATTCGATTTTCAGGAACCTCAGCTTATATGCGGTAAAAAGTTTGAATCAG  
CCTGTGTTCTTCAAGTTCGCTCTCCAGTCACATCTCCAGAAAAAGCTGAGAGACATT  
20 ACTTTGACTGCAAGTTGTGTGCTTCTATAATCTTATCTTGGAGCAATGGTTATGTAT  
CATCACCATCGCGTCCGAGAACCAATACGACATCTTTTGTAGTAGCTGGGGAAGAT  
GACAGGAAGATTTCCTTTGGACAACATAAAGCATCTCTTTACGTGAAATCCAGCTCGCA  
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTGGTAAAGTATACAGA  
GGTTTGCTTCCAGACAAAAAAAAGTTGCAGTGAACGCTTGCGGATTACTCTAGTCTCT  
25 GGAGGAGAAGCTGCTTTCCAAAGAGAGATTCACTCATAGCGTTGCGGTTCATAAAAAAT  
CTCTTACGCCTTATGGCTTCTGCACAACCTCTCTCTGAGAGATCTCTGTTTATCCATAC  
ATGGAATACTTAGTGTTCATATCGACTAAGAGATTGAAAGCGGAGAGGAAGGATTA  
GACTGGCCCAACAGGAAGCGGTAGCTTTTGGTTCAAGCTCAAGGTTTAGAGTATCTACAC  
GAACATTGTAACCCGAAGATCATACCGCGATCTCAAGGCTGCAAAACATACCTTTAGAC  
30 AACAAATTTGAGCCAGTCTCTGGAGATTTCGGTTTAGCTTAAGCTTGGGACACATCTCTG  
ACTCATGTCACAACTCAAGTCGAGGCAACATGGGTACATTGCGCCAGAGTATCTCTGC  
ACAGGAAAAATCATCTGAAAAAACCGATGTTTGTGTTACGGTATAACGCTTCTTGAGCTT  
GTTACTGGTCAGCGCGCAATCGATTTTCAAGCTTGAAGAGAGGAAAAATATTCTCTTG  
CTTGATCATATAAAGAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT  
35 TTGACTACATATGACTCCAAAGAAGTTGAACAATCGTTCAAGTGGCTCTCTCTGCACA  
CAAGGCTCACCAAGATAGACCAGCGATGTCTGAAGTGGTCAAAATGCTTCAAGGGACT  
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACAACCTTGAAGAAGTTAGGAACAAGAA  
GCATTGTTGCTTCCGACTTTACCGGCTACTTGGGATGAAGAAGAAACACCGTTGATCAA  
GAATCTATCCGATTATCGACAGCAAGATGAagaagaacagagagagaaagatatctatg  
40 aaaa (SEQ ID NO: 44)

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a  
10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each  
15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular  
20 domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth  
25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSTTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLs

P AITKLKFLVTLELQNNLSLGA

PDLSLGNMVMNLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI  
PTQFFSIPTFEFSGTQLCGKS

5 LNQPCCSSRLPVTSSKKKLAD

ITLTASCVASIIL  
FLGAMVMYHHH

10

RVRRTKYDIFFDVAGEDDR  
KISFGQLKRFSLREIQLAT

DSFNESNLIGGGFGKVYRGLLPD

15

KTKVAVKRLADYFSPGGEAAQ  
REIQLISVAVHKNLLRLIGFCT  
TSSERILVYPYMENLSVAYRLR  
DLKAGEEGLDNPTKRKRVAFGSA  
HGLEYLHEHCNPKIIHRDLKAA

20

NILLDNNFEPVLGDFGLAKLVD  
TSLTHVTQVRGTMGHIAPEYL  
CTGKSSEKTDVFGYGITLLELV  
TGQRAIDFSRLEEEENILLDD  
HIKKLLREQRLDIVDSNLTTY

25

DSKEVETIVQVALLCTQGSPEL  
RPAMSEVVEMLQ

GTGGLAEKWTEWQLEEVNRKEALLL

30 PTLPATWDEETTVDQESIRLSTAR (SEQ ID NO: 45)

*Arabidopsis thaliana* RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 tottccttctccttctggaataataatctaaagcttttc**ATGGTGGT**GATGAAGATATTC  
 TCIGTTCTGTTACTACTATGTTTCTCGTTACTTGTTCTCTCTCTCTGAACCCAGAAAC  
 CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC  
 AAAAATGGGATGAGTTTCTGTTGATCCTTGATGCTGGACTATGATCTCTTGTCTTCA  
 GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTTCAGGAACCTTATCTGGG  
 15 TCTATTGGAAATCTACTAATCTTCGACAAGTGTCAATACGAACAATAACATCTCCGGT  
 AAAATCCCACCGAGATTGTCTCTCCCAAATTACAGACTCTGGATTATCCAATAAC  
 CGGTTCTCCGGTGAATCCCGGTTCTGTTAACAGCTGASTAATCTCCAATATCTGTTG  
 AACACAACATCATTATCTGGGCCCTTTCTGCTTCTCTGTCTCAAAATCCCTCACTCTCT  
 TTCTTAGACTTGTCTTATAACAATCTCAGAGTCTCTGTTCCATAAATTCCTGCAAGGACA  
 20 TCAATGTCTGGGAACCCCTTGATTGTTAAAAACAGCCTACCGGAGATTGTTTCAGGA  
 TCAATCAGTGCAGGCCCTCTTTCTGTCTTTACGTTCTTCATCAGGACGTAGAACCAAC  
 ATATTAGCAGTTGCATCTGGTGTAAAGCCTTGGCTTTGCTGTTAGTGTAACTCTCTCTCTC  
 GGGTCATTGTTGGTATCGAAAGAAACAAAGACGGTTAACGATGCTTCGCAATTAACAGCAA  
 GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAAAGCTTCACATTGAGGAACTTCATGTA  
 25 GCTACGGATGGTTTTAGTTCOAAGAGATTCTTGGTGTCTGGTGGGTTTGGTAACTGTCTAC  
 AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAACGATTGAAGATGTGAATGGA  
 ACCCTCCGGGAATCAGAGTTTGTGACTGAGCTTGAGATGATCAGCTTAGCTGTTATAGG  
 AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCCCT  
 TACATGTCCAATGGCAGCGTCGCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAGA  
 30 ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGCAATGC  
 GATCCCAAGATTATTCACCGAGATGTCAAGGCAGCAACATCTCCTAGATGAGTATTTT  
 GAAGCAGTTGTTGGGATTTTGGACTACAAAGCTACTCAACCAGAGGATTCACATGTCT  
 ACACCCGCGGTTAGAGGAACTGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCAG  
 TCATCTGAGAAACCGATGTCTTTGGGTTCCGTATACTTTTGCTAGAGCTCATCACAGGA  
 35 ATGAGAGCTCTCGAGTTTGGCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAAATGGGTG  
 AGGAAGCTACACAGGAAATGAAGTAGAGGAGCTAGTAGACGAGAACTGGGGACAACC  
 TACGATAGAAATAGAAGTTGGAGAGATGCTACAAGTGGCAGCTGCTCTGCATCAGTTTCTT  
 CCAGCTCACAGACCCAAATGTCTGAAGTAGTTAGATGCTGAAGGAGATGGATTAGCT  
 GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTTACAGG  
 40 ACTATTACCTCTACTGATGCCAACCAACCAACCAACATCTGTTGGCTCCTCAGGATTT



GAAGATGAAGATGATAATCAAGCGTTAGATTTCATCGOCATGGAACATATCTGGTCCAAGG

TAGtaaatcttggacacagaaagaaacagatataatatccccatgacttcaattttgtt (SEQ ID NO: 46)

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
- 20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MVVMKLITMKIFSVLLLL  
CFFVTCSLSSEPRNPEV

EALINIKNELHDP

35

HGVFKNWDEFSVD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI  
PPEICSLPKLQTLDLNNRFSGEI  
PGSVNQLSNLQYLRLLNNNSLGGPF  
5 PASLSQIPHLSFLDLSYNNLRGPV  
PKFPARTFNVAGNPLICKNS

LPEICSGSISASPL  
SVSLRSSGRRTN

10

ILAVALGVSLGFAVSIL  
SLGFIWY

RKKQRRLTMLRINKQEE

15

GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFQNVYRGKFGD

GTVVAVKRLKDVNGTSGNSQFR

TELEMISLAVHRNLLLELIGYCA

20

SSSERLLVYPYMSNGSVASRLK

AKPALDWNTRKKIAIGAA

RGLFYLHEQCOPKIIHRDVKAA

NILLDEYFEAVVGDFGLAKLLN

HEDSHVTTAVRGTVGHIAPEYL

25

STGQSSEKTDVFGGILLELI

TGMRALEFGKSVSQKGAMLEW

VRKLHKEMKVEELVDRELGTYY

DRIEVGEMLQVALLCTQFLPAH

RPKMSEVVQMLE

30

GDGLAERWAASHDHSHFYHANM

SYRTITSTDGNNQTKHLFG

SSGFEEDDNQALDSFAMELSGPR (SEQ ID NO: 47)

35

*Arabidopsis thaliana* RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 ctagagaattcctatactttttctacg**ATGGAGATTCTTTGATGAAGTTCTCTGTTT**  
 GGAATCTGGGTTTATTACTCTGTTCTTGACTCTGTTCTGCCATGGATAGTCTTTTA  
 TCTCCCAAGGTGGCTGCGTTAATGTCAGTGAAGAACAGATGAAAGATGAGAAGAGGTT  
 TTGCTGGTTGGGATATTAACTCTGTTGATCCTTGTAATGGAACATGGTTGGTTGTTCT  
 TCTGAAGGTTTGTGTTCTCTAGAGATGGCTAGTAAAGATTATCAGGATACTACTCT  
 15 ACTAGTATTGGGAATTAACATCATCTTCACTACTTGTACTTCAGAATAATCAGTTAACT  
 GGTCCGATTCTTCTGAGTTAGGCCAACTCTCTGAGCTTGAACGCTTGATTATCGGGG  
 AATCGGTTTAGTGGTGAATCCAGCTTCTTTAGGGTCTTAACCTACTTAACTACTTIG  
 CGGCTTAGCAGGAATCTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT  
 CTTCTTTCTTGGAATCTATCTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA  
 20 AAAGATTACAGGAATGCATTTCTTTGTTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC  
 TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT  
 AGCAAAACATCAGCCTTAGTGCTCTCTTTTGCAATTTGGCATTTGTTGTCCTTATCATC  
 TCCCTAATGTTTCTCTTCTTCTGGGTGCTTTGGCATCGATCAAGTCTCTCAAGATCACAC  
 GTGCAGCAAGACTACGAATTGAAATCGGCCATCTGAAAAGGTTCAGTTTTCGCGAAATA  
 25 CAAACCCCAACAAGCAATTTTAGTCCAAAGAATTTTGGACAAGGAGGGTTTGGGATG  
 GTTTATAAAGGGTATCTCCAAATGGAATCTGTTGGTGGCAGTTAAAAGATTGAAAGATCCG  
 ATTTATACAGGAGAAGTTCAAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTTAC  
 CGTAACCTTTTACGCCCTTTTGGATTCTGTATGACCCCGGAAGAGAGAATGCTTGTGTAT  
 CCGTACATGCCAAATGGAAGCGTAGCTGATGCTGAGAGATTGGAATCGGAGGATAAGC  
 30 ATTGCACTCGGCGAGCTCGAGGACTTGTTTACTTGCAAGCAATGCAATCCAAAGATT  
 ATTCACAGAGACGTCAAAGCTGCAAAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT  
 GCGGATTTTGGCTAGCAAAAGCTTTTAGACCAGAGAGATTCACATGTCACTACCGCAGTC  
 CAGGGAACCAATTGGACACATCGCTCCGAGTACCTTTCCACTGGACAGTCTCTCAGAGAAA  
 ACCGATGTTTTCGGATTTCGGAGTACTAATCCTTGAACCTATAACAGGTGATAAGATGATT  
 35 GATCAAGGCAATGGTCAAGTTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA  
 GCAGAGAAGAGATTTCGAGAGATGGTGGACAGAGATTGGAAGGGAGAGTTTGATGATTTG  
 GTGTTGAGGAGAGTAGTGAATTGGCTTTGCTTTGTACACAGCCATCCGAATCTAAGA  
 CCGAGGATGCTCAAGTGTGAAGGTAAGAGGTTTAGTGAACAGTGTGAAGGAGGG  
 TATGAAGCTAGAGCTCCAAGTGCTCTAGGAACACAGTAATGGTCATGAAGAGCAGTCC  
 40 TTTATTATTGAAGCCATTGAGCTCTCTGGACCAAGATGATagacttcatagtgtcttaac

tagtctctcttgattttgtgtcattgtcatggc (SEQ ID NO: 48)

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

- At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
- 15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine /
- 20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
- 25 protein interactions.

MEISLMKFLFLGIWVYYYIS  
VLDSVSAMDSLLSPKV

30

AAIMSVKNMKMDE  
KEVLSGWDINSVD

PCTWNMVGCSSEGFVVS

35

LEMASKGLSGILS  
T SIGELTHLHTLLQNNQLTGPI  
PSELGQLSELETLDLSGNRFSGEI  
PASLGFLTHLNLRLSRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT  
PNISAK DYRKICISLWSSFPR

ALLRCYTCEKCCNR

5 SAATGLSEKDNSK

HESLVLSTAFGIVV  
AFIISIMFLFFWVLWH

10 RSRLSRSHVQQDYEF  
EIGHLKRFSFREIQTAT

SNFSPKNILGQGGFMVYKGYLPN  
GTVVAVKRLKDFIYTGEVQFQ

15 TEVEMIGLAVHRNLLRLFQFCM  
TPEERMLVYPYMPNGSVADRLR  
DWNRRISIALGAA

RLVYLHEQCNPXIHRDVKAA  
NILLDESFEIIVGDFGLAKLLD

20 QRDSHVTTAVRGTIIGHIAPEYL  
STGQSSEKTDVFGVLEILELI  
TGHKMIDQNGQVRKGMILSW  
VRTLKAEKRFAEMVDRDLKGEF  
DDLVEEVVELALLCTQPHPNL

25 RFRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFIEAIELSGPR (SEQ ID NO: 49)

30

*Arabidopsis thaliana* RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
attgtttcctctctttgggattttctccttggatggaaccagctcaattaatgagatgag
10 ATGAGAATGTTTCAGCTTGCAGAAGATGGCTATGGCTTTACTCTCTGTTTTTTCGCTGT
TTATGCTCATTGTGTCTCCAGATGCTCAAGGGGATGCAGTGTTCGGTTGAGGATCTCC
TTAGCTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTAATTTGTGATGACAAAAACTTTTGCTACTTCTCTACATTGTGATGATTA
AAGTTCTCGGGAACTTGTCTTCAAGAGTAGGAATCCTAGAAAAATCTCAAGACTCTTACT
15 TTAAGGGAAATGGAATACGGGTGAAATACCAAGAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTTGGAGGACAATCAGCTAACTGGTGCATACCATCCACTATCGGTAAT
CTCAAGAACTTCAGTTCTTGACCTTGAGTAGGAACAACTTAATGGGCACTATTCGGGAG
TCAGTCACTGGTCTTCCAAACCTGTTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCCCTCAAAGTCTGTTTGAGATCCCAAAATATAATTACAGTCAAACAACTTGAAT
20 TGTGGCGGTGCTCAACCTCACCTTGTGTATCCGCGGTTGCCATTGAGGTGATCAAGC
AAGCTTAAACTGGCATTATGTCTGGAGTTGTGTCTGGAGTTACAGTTGTCTCTTTTGA
ATCTTGTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTGTG
GATGTTGCAAGTGAAGTGGACAGGAGAATTGCAATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAAATGTACTTGTGTCAGGAGGC
25 TTTGGGAAAGTTTACAAGGAGTGTCTCCGGATACACCCAAGTTGCTGTGAAGAGATTG
ACGGATTTGCAAGTCTCGTGGAGATGCTGCTTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTCAAGGAATCTACTCCGTCTTACGGGTTCTGCACCAACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGACATCGCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAACGGAATGCCTTAGGAGCRGCGCT
30 GGTTTTGAGTATCTTCATGAACATTGCANTCCGAAGATCATACATCGTGAATGAAAGCA
GCTAATGTGTACTAGATGAAGATTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAAG
TAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTGAGGAAACAAATGGGTCAATT
GCACCAAGAAATTTATCAACAGGGAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTACAGGACACACGCGCAATAGACTTTTACGTTTGGAGGAA
35 GAAGATGATGCTTGTACTTGAACACGTGAAGAACTGGAAGAGAGAGAAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAGAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTTCAACAGAGACGCCACAGTGAATGCTGAAGTT
GTGAGGATCTTGAAGGAGAGGGCTTGGGAGAGATGGGAGAGTGGCAAAACGTGGAA
GTCACGAGACGTGATGAGTTTGAACGGTTGCAGAGGAGATTGATTGGGGTGAAGATCTT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGAAGATGaccaaaaacatcaaacctt (SEQ ID NO: 50)
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus  
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each  
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain  
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown  
20 function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single  
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAFITLLFFACLCSEFVSPDAQG

30

DALFALRISLRALP

NQLSDWNQNVN

PCTWSQVICDDKNFVTSL

35

TLSDMNFSGTLSSRV

GILENLKTLTLKGNIGITGEI

PEDFGNLTSLTSLDLEDNQLTGRI

PSTIGNLKKLQFLTLSRNKNGTI  
PESLTGLPNLLNLLDSNLSGQI  
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTVVL  
FGILLFLFC

10 KDRHKGYYRDRVFDVAGE  
VDRRIAFGQLKRFARRELQLAT

DNFSEKNVLGGGFGKYKGVLPD  
TPKVAVKRLTDFESPGDAAFQ  
15 REVEMISVAVRRNLLRLIGFCT  
TQTERLLVYFFMQNLSLAHRLR  
EIKAGDPVLDWETRKRIALGAA  
RGFEYLHERCNPKIHRDVKAA  
NVLLDEDFEAVVGDFGLAKLVD

20 VRRTNVTTQVRGTMGHIAPEYL  
STGKSSERTDVFGYGIMLLELV  
TGQRAIDFSRLEEEDVLLLDH  
VKKLEREKRGLAIVDKNLDGEY  
IKEEVENMIQVALLCTQGSPEL

25 RPVMSEVVRMLE

GEGLAERWEWQNVETTRHEFE

RLQRRFDWGEDSMRNQDAIELSGGR (SEQ ID NO: 51)

30



*Arabidopsis thaliana* RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 acatcttggttttctgctcattcctctgtttcaaca**ATGGAGAGTACTATTGTTATGATGA**  
 TGATGATAACAAGATCTTTCTTTTGCTCTTGGGATTTTATGCCTTCTGCTCTCTG  
 TTCACGSATGCTTTCTCCTAAGGTGTTAACTTTGAAGTGAAGCTTTGATGGACATAA  
 AGCTTCATTACATGATCCTCATGGTGTCTTGATAACTGGGATAGAGATGCTGTTGATC  
 CTGTAGTTGGACAATGGTCACTTGTTCTTCTGAAAACCTTTGTCATTGGCTTAGGCACAC
- 15 CAAGTCAGAAATTTATCTGGTACACTATCTCCAAGCATTACCACTTAACAAATCTTCGGA  
 TTGTGCTGTTGCAGAACAAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA  
 CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTCCAOGGTGAAATTCCTTTTTCAG  
 TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAAATCTCTCTCTGGAGTGT  
 TTCTCTGTCACTATCTAATATGACTCAACTTGCCCTTCTTGATTATCATACAACAATC
- 20 TATGGTCTCTGTTCCAAGATTTGCTGCAAGACGTTAGCATCGTTGGGAACCCGCTGA  
 TATGTCCAACGGGTACCGAACCAAGACTGCAATGGAACCAATGATACCTATGCTATGA  
 ACTTGAATCAAACCTGGAGTTCCTTTATACGCCGGTGGATCGAGGAATCACAAATGGCAA  
 TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATGCTGTTGGTTTGTTC  
 TCTGTTGGAGACAAAGACATAACCAAAACACATCTTTGATGTTAAAGATGGGAATCATC
- 25 ATGAGGAAGTTTCACTTGGAAACCTGAGGAGATTGGTTTCAGGGAGCTTCAGATTGCGA  
 CCAATAACTTCAGCAGTAAGAACTTATGGGGAAGGTGGCTATGGAATGTATACAAG  
 GAATACTTGGAGATAGTACAGTGGTTGCAGTGAAGAGCTTAAAGATGGAGGACATTGG  
 GAGGAGAGATTCAGTTTCAGACAGAAGTTGAATGATCAGTTTAGCTGTTTCATCGAAATC  
 TCTTAAGACTCTACGGTTTCTGCATCACAAACTGAGAAGCTTCAGTTTATCCTTATA
- 30 TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGACTGGAGCATAA  
 GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC  
 CGAAGATTATCCACCGCGATGTCAAAGCAGCGAATATATCTTGTGACTACTGTGAAG  
 CTGTGGTTGGCGATTTTGTTTAGCTAAACTCTTGGATCATCAAGATTCTCATGTGACAA  
 CGCGGTTAGAGGCACGGTGGTGCATTGCTCAAGATATCTCAACTGGTCAATCTCT
- 35 CTGAGAAAAAGATGTTTTGGCTTCGGGATTCCTCTCTTGAGCTTGTAACCGGACAAA  
 GAGCTTTTGAGTTTGGTAAGCGGCTAACCAAGAGGTGTGATGCTTGATTGGGTAAAAA  
 AGATTATCAAGAGAAGAACTTGAGCTACTTGGGATAAAGAGTTGTTGAAGAAAGA  
 GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTGTGCACAGATACC  
 TGCCAGGCATAGACCAAAAATGTCTGAAGTTGTTGGAATGCTGGAAGGAGATGGACTTC
- 40 CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG  
 TGCAGGCAATGGAGCTCTCTGGTCTAGATGAaatctatacatgaatctgaagaagaaga  
 agaacatgcacatctgtttcttgaatcaagagggaattcttgttttttggataatagagagg  
 tttttggagggaatgttgtctctgtaactgtataggcttgtgtgtaagaagttaa  
 5 tactgcacttagggtaattcaaaagttctttacataaaaaatgattagttgcgttgaata  
 gaggggaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaa (SEQ ID NO: 52)

- 10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

- 15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate  
 20 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-  
 25 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably  
 30 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF  
 CFIQFLCLLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP  
HGVLNWDNRDAVD

PCSWTMVTCSSNFVIG

5

LGTPSQNLSGTL  
SPSITNLTNLRIVLLQNNNIKGI  
PAEIGRLTRLETLDLSDNFFHGEI  
PFSVGYLQSLQYLRLNNSLSGVF  
10 PLSLSNMTQLAFLDLSYNNLSGPF  
PRFAA KTFSIVGNPLICPT

GTEPCNGTTLIPMSMNL  
NQTGVPLYAGGSRNHKMA

15

IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKGDNHHE  
EVSLEGNLRRFGFRELQIAT

20

NNFSSKNLLGKGYGNVYKGILGD  
STVVAVKRLKDGALGGEIQFQ  
TEVEMISLAVHRNLLALYGFCI  
TQTEKLLVYPYMSNGSVA

25

SRMKAKPVLDSIRKRIAIGAA  
RGLVYLHEQCDPKIHRDVKAA  
NILLDDYCEAVVDGFLAKLLD  
HQDSHVTTAVRGTVGHIAPEYL  
STGQSSEKTDVFGFGLLLELV

30

TGQRAFEFGKAANKQGVMLDW  
VKKIHQEKLELLVDKELLKKKSY  
DEISLDEMVRVALLCTQYLPGH  
RPFMSEVVVRMLE

35

GDGLAEKWEASQRSDS  
VSKCSNRINELMSSS

DRYSDLTDDSSLLVQAMELSGPR (SEQ ID NO: 53)

40

*Arabidopsis thaliana* RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 gttttttttttttaccctcttgaggagatctgggaggagaaattgcttttttttgtaa  
 ATGGGAGAAAAAGTTTGAAGCTTTTGGTTTGTCTGCTTAATCTCACTGCTTCTCTCG  
 TTTAATTCGTTATGGCTTGCCCTCTTCTAACATGGAAGTGATGCACGTCACAGTTTGAGA  
 GCTAATCTAGTTGATCCAAATAATGTCTTGCAAGCTGGGATCTACGCTTGTTAATCCG  
 TGTACTTGGTTTCACGTAACGTGTAACAACGAGAACAGTGTATAAGAGTCGATCTTGGG  
 15 AATGCAGACTTGTCTGGTCAGTTGGTTTCCTCAGCTAGTTCAGCTCAAGAACTTGCAGTAC  
 TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTTCCAAGCGATCTTGGGAATCTGACA  
 AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA  
 GAAAGCTATTCAAGCTTCGCTTTCTTCGGCTCAACATAACAGTCTCAACGACCAAAAT  
 CCGATGTCATTGACTAATAATCATGACCTTCAAGTTTGGATCTGTCGAACAACCGATTA  
 20 TCCGATCTGTTCTCTGATAATGGTTCTTCTCGCTCTTCACTCCCATCAGTTTGTCTAAC  
 AACTTGGATCTATGCGGCCAGTTACTAGCCGCTCTTGTCTTGGATCTCCCCCGTTTTCT  
 CCTCCACACCTTTTATACCACTCCCATAGTTCTTACACCAAGTGGGTATAGTGCTACT  
 GGAGCCATTGCGGGAGAGTTGCTGTGTGCTGCTTTACTATTGTGCTCCCTGCTTTA  
 GCTTTTGTGTTGGTGGCTAGAAGAAACCTCAAGAAITCTTCTTTGATGTTCTGCGGAA  
 25 GAGGACCTTGAGGTTCACTTGGGCGAGCTTAAAGCGTTTCTCTACGGGAATCTCAAGTA  
 GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCGAGGTGGGTTCGAAAAGCTCTAC  
 AAAGGCGCTTGTGATGGAACACTTGTGCACTCAACCGCTTAAAGAGAGCGAACC  
 CCAGGTGGGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTTCACAGA  
 AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGTATTCTCT  
 30 TACATGGCTAAATGGAAGTGTGCTTCTGTGTGAGAGAACGTCACCATCACAGTTGCCT  
 CTAGCCTGCTCAATAGACAGCAATCGCGCTAGGATCAGCGAGGGGTTGTCTTATCTTT  
 GATGATCATTTGCGACCCCAAAATATTACACGCTGATGTGAAAGCTGCTAATATTCTGTG  
 GACGAGGAATTTGAGGCGGTGGTAGGTGATTTCCGGTTAGCTAGACTTATGAGACTATAAA  
 GATACTCATGTACAAACGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC  
 35 TCACTGGAATACTCTCAGAGAAAAGTATGTTTTGGCTACGGATCATGCTTTTGGAA  
 CTGATTACAGTTCAGAGAGCTTTTGATCTTGCAAGACTGGCGAATGACGATGACGTTATG  
 CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCTC  
 GACCTGCAAGAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC  
 TGCACACAGAGCTCACTATGGAACGACCTAAGATGTCTGAGGTGTTTGAATGCTTGAA  
 40 GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTCTCACCCACCTCTGACTGGATCCTTGATTCGACTGATAATCTTCAT  
GCTATGGAGTTGTCCTGGTCCAAGATAAacgacattgtaatttgctaacagaaaagagaa  
agaacagagaaaatattaagagaatcacttctctgtattctt (SEQ ID NO: 54)

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt *et al.* 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGFVCLISLLLLFNSL  
WLASNMEG

DALHSLRANLVD  
NNVLQSWDPTLVN

35 PCTWFHVTCNNNSVIRV

DLGNADLSGQLV

P QLQQLKNLQYLELYSNNITGPV  
40 PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGKLFKLRFLRLNNSLTGPI  
PMSLTNIMTLQVLDLSNNRLSGSV  
PDNGSFSLEFTPISFANNLDLGGPV

5   TSRPCPGSPPFSPPPP  
     FIPPPIVPTGGYSATG

     AIAGGVAAGAAL  
     LFAAPALAFANW

10       RRRKPEFFFDVPAEDPE  
         VHLGQLKRFSLRELQVAT

         DSFSNKNILGRGGFGKVKYKRLAD  
15   GTLVAVKRLKEERTPGGELQFQ  
     TEVEMISMVHRNLLRLRGFCM  
     TPTERLLVYPYANGSVASCLR  
     ERFPSQLPLAWSIRQQIALGSA  
     RGLSYLRHDHCDPKIHRDVKAA

20   NILLDEEFVAVGDFGLARLMD  
     YKOTHVTTAVRGTIIGHIAPEYL  
     STGKSSEKTDVFGYGIMLELI  
     TGQRAFDLARLANDDDVMLLDW  
     VKGLLKEKKLEMLVDPDLQSNY

25   TEAEVEQLIQVALLCTQSSPME  
     RPMSEVVRMLE

     GDGLAEKWDEWQKVEVLRQEVELS

30   SHPTSDWILDSTONLHAMELSGPR (SEQ ID NO: 55)

*Arabidopsis thaliana* rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggggttttaacaatgatggattttctctgatgagggatgttcttaggggttgtttt  
taatctcttgaggataaaATGGAACGAAGATTAAATGATCCCTTGCTCTTTTGGTTGATT  
CTCGTTTGGGATTGGTTCTCAGAGCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA  
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT  
ACTCCATGTACATGGTTTTCATGTTACTTGCAATAGCGACAATAGTGTACAGGTGTGAC  
15 CTGGGAATGCAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAAACCTG  
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAAGACAGCTTGGAAAT  
CTGACGGAAATGGTGAGCTTGGATCTTTACTTGAACAATTTAAGCGGGCCTATTCCATCA  
ACTCTCGGCCGACTTAAGAACTCCGTTTCTTGGCTCTTAATAACAATAGCTTATCTGGA  
GAAATTCGAAGGTCTTTGACTGCTGTCTGACGCTACAAGTTCTGGATCTCTCAACAAT  
20 CCTCTACCCGAGATATTCTGTTAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT  
GCCAACACCAAGTGACTCCCCCTTCTGCACTCCACCGCTCCTATCTCTCTACACCG  
CCATCACCTGCAAGGAGTAATAGRAATTACTGGAGCGATTGCGGGAGGAGTGTCTGCAAGT  
GCTGCACTTCTAATTGCTGTTCCGGCCATTGCACTAGCTTGGTGGCGAAGGAAAAGCCG  
CAGGACCACTTCTTTGATGTACAGCTGAAGAGGACCAGAGTTCATTTAGGACAACTG  
25 AAGAGGTTTTCAATGCGTGAACACAAAGTTGCTTCGGATAATTTAGCAACAAGACATA  
TTGGGTAGAGGTGGTTTGGTAAAGTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG  
GCCGTTAAAAGGCTAAAAGAGGAGCGCACCCAGGTGGCGAAGTGCAGTTCCAGACAGAG  
GTGAGATGATAGTATGGCGGTTACAGAACTTGCTTCGGCTTCGGGATTTTGATG  
ACTCCAACCGAAAGATTGCTTGTATTATCCTACATGGCTAATGGAAGTGTTCCTCTGT  
30 TTAAGAGAACGTCCGAGTCCCAAGCCACACTTGATTGGCCAAAGAGACAGCGTATTGCG  
TTGGGATCTGCAAGAGGGCTTGCATTTACATGATCATTTGCGACCCAAAGATATTATCAT  
CGAGATGTGAAGCTGCAAAATATTTTGTGGATGAAGAGTTTGAAGCCGTGGTGGGAT  
TTTGACTTGCAAAATCTATGCACTACAAAGACACACATGTGACAACCGCAGTGCCTGGG  
ACAATGGTCATATAGCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAACCGAT  
35 GTCTTTGGGTATGAGTCAATGCTTCTTGAGCTTATCACTGGACAAGGGCTTTTGATCTT  
GCTCGCTCGCAAGATGATGATGATGTCATGTTACTAGACTGGGTGAAGGGTTGTAAAA  
GTGAAGAATTTGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAGACGAAGAA  
GTGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGATTCACCAATGGAAGACCC  
AAATGTCTGAAGTTGAAGAATGCTTGAAGGAGATGGTTAGCTGAGAGATGGGAAGAG  
40 TGGCAAAAGGAGAAATGTTCAAGACAGATTTCACACTACCAACCCACCATCCAGCCGTG

TC TGGCTGGATCATTGGCGATTCCACTTCCAGATOGAAAAAGAAATACCCCTCGGGTCCA  
AGATAA gattogcaaacacgaatgtttttctgtattttgttttctctgtattattgag  
ggttttagcttc (SEQ ID NO: 56)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS10 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a  
signal sequence. The second domain contains a leucine zipper motif,  
containing 4 leucine residues, each separated by seven other amino  
15 acids. The third domain contains conserved cysteine residues,  
involved in disulphate bridge formation. The fourth domain contains a  
leucine rich repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain contains many  
serine and proline residues, and is likely to contain hydroxy-proline  
20 residues, and to be a site for O-glycosylation. The sixth domain  
contains a single transmembrane domain after which the predicted  
intracellular domains are positioned. The seventh domain has an  
unknown function. The eighth domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably also  
25 containing sequences for protein / protein interactions. The ninth  
domain has an unknown function. The last and tenth domain at the C-  
terminal end represents part of a single leucine rich repeat,  
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL  
DLVLRVSGNAEG

DALSALKNSLADP  
NKVLQSWDATLVT

35

PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV

M QLQQLPNLQYLELYSNNTGTI

40

FEQLGNLTSLVSLDLYLNNLSGPI



PSTLGRLLKRLRLNNSLSGEI  
PRSLTAVLTQLVLDLSNNPLTGDI  
PVNGSFSLTPISFANTK IT PL

5 PASPPPFISPTPPSPAGSNRITG

AIAGGVAAGAAL  
LFAVFAIALAWW

10 RKKKPDHFFDVPAAEDPE  
VHLGQLKRFSRLRELQVAS

DNFSNKNILGRGGFGKVYKGRLLAD  
GTLVAVKRLKEERTQGGEIQFQ

15 TEVEMISMAVHRNLLRLRGFCM  
TPTERLLVYPYANGSVASCLR  
ERPESQFPPLDWPKRQRIALGSA  
RGLAYLRDHCDPKIHRDVKAA  
NILLDEEFVAVGDFGLAKLMD

20 YKDTHTTAVRGTIHIAPEYL  
STGKSSEKTDVFGYGVMLLELI  
TGQRAFDLARLANDDDVMLLDW  
VKGLLKEKKLEALVDVQLQNY  
KDDEVEQLIQVALLCTQSSPME

25 RPKMSEVVRMLE

GDGLAERWEENQKEMFRQDFNYPTHH

PAVSGWIIGDSTSQIENEPYSGPR (SEQ ID NO: 57)

30

*Arabidopsis thaliana* RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 ttgttaacctctcgtactaaaaattctccATGGTAGTAGTAACAAAGAAGACCATGAAGA  
TTCAAATTCACTCCTTTACTCGTTCTTGTCCTCTGTTCTCTACTCTCACTATCTTT  
CTGAGCCCGAAAACCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTGCATGATC  
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTCAGTTGATCCTTTAGCTGGGCTATGA  
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGGCGCGAGCCAGTCTCTCTCGG  
15 GAGGTTTATCTGAGTCTATCGSAAATCTCACAATCTCCGACAAGTGTCATTGCAAAATA  
ACAACATCTCCGGCAAATTCACCGGAGCTCGGTTTCTACCCAAATTACAACCTTGG  
ATCTTTCCAACAACCGATTCTCCGCTGACATCCCTGTTCCATCGACCAGCTAAGCAGCC  
TTCATATCTGAGACTCAACAACAACCTTTTGCTCGGGCCCTTCCTGCTTCTTTGTGCC  
AAATTCCTCACTCTCCTTCTTGGACTTGTTTACAACAATCTCAGTGGCCCTGTTCTCTA  
20 AATTCCGACGAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTGTAGAAGCAACCCAC  
CTGAGATTGTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT  
CAGGACGCAAGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTGTGTA  
TACTAGTCTTGCCTCTCGGGTCTCTTTGTTGGTACGAAAGAAACAAGAAGGCTACTGA  
TCCTTAACCTTAAACGAGATAAACAAGAGGAAGGGCTTCAAGSACTTGGGAATCTAAGAA  
25 GCTTCACATTGAGAGAACTCCATGTTTATACAGATGTTTCAGTCCAGAACAATCTCG  
GCGCTGGTGGATTGCGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG  
TGAACCGTTGAAGGATATTAAATGGAACCTCAGGGGATTCACAGTTTCGTATGGAGCTAG  
AGATGATTAGCTTAGCTGTTCAAGAATCTGCTTCGGTTAATGGTTATTGCGCAACTT  
CTGGTGAAGGCTTCTTGTTTACCCCTTACATGCTAATGGAAGCGTCGCTCTAAGCTTA  
30 AATCTAAACCGGCATTGGACTGGAACATGAGGAAGGAGTAGCAATTGGTGACGAGAGAG  
GTTTGTGTATCTACATGAGCAATGTGATCCCAAGATCATTATAGAGATGTAAGGCGAG  
CTAATATTCTTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAGC  
TCCCTTAACCATCGGGAATCTCATGTCCAACTGCGGTCGGTGTAAGGTTGGCCACATTG  
CACCTGAATATCTCTCACTGGTCAGTCTCTGAGAAACCGATGTGTTGGGTTCGGTA  
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAACCGTTAGCC  
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAGTAGAGGAAC  
TATTGGATCGAAGACTCGGAACCTAATACGATGAAGATTGAAGTTGGAGAGATGTTGCAAG  
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATGCTCTAAATGTCTGAAGTTGTTT  
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCAATTCACATT  
40 TCTACCATGCCAATATCTCTTTCAAGACAATCTCTCTCTGTCTACTACTCTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACCTTATCAAATGTTTGATCTTCGGCTTTCGATG  
ATGACGATGATCATCAGCCTTTAGATTCTTTGCCATGGAACATCCGGTCCAAGATAAc  
acaatgaaagaaagatatcatctttttacgatggatcaacaatccaatgaaaaaa (SEQ ID NO: 18)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS11 protein.

- 10 Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 3 leucine residues, each  
separated by seven other amino acids. The third domain  
contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each

- 20 approximately 24 amino acid residues. The fifth domain  
contains many serine and proline residues, and is likely to  
contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
function. The eighth domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
30 domain at the C-terminal end represents part of a single  
leucine rich repeat, probably involved in protein / protein  
interactions.

MVVVTKRTMKIQIHLLYSFLFL

- 35 CFSTLTLSSEPRNPEV

EALISIRNNLHDP

HGALNNWNEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5   ESIGNLTNLRQVSLQNNNISGKI  
PPELGFLPKLQTLDSLNNRFSGDI  
FVSIQQLSSLQYLRNNNSLSGPF  
PASLSQIPHLSFLDLSYNNLSGPV  
PKFPARTFNVAGNPLICRSN

10

PPEICSGSINASPL  
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL

15

VLALGSFCWY

RKKQRLLILNLNGADKQEE  
GLQGLGNLRSFTFRELHVYT

20

DGFSSKNILGAGGFGNVYRGKLG  
GTWVAVKRLKINGTSGDSQFR  
MELEMISLAVHKNNLLRIGYCA  
TSGERLLVYPMPNGSVASKLK  
SKFALDWNMRKRIAIGAA

25

RGLLYLHEQCDFKIIHRDVKAA  
NILLDECFAVVGDFGLAKLLN  
HADSHVTTAVRGTVGHIAFEYL  
STGQSSEKTDVFGFGILLLELI  
TGLRALEFGKTVSQKGAMLEW

30

VRKLHEEMKVEELLDRELGTNY  
DKIEVGEMLQVALLCTQYLPAN  
RPKMSEVVLMLE

GDGLAERWAASHNHSHFYHANI

35

SFKTISLSTTSVSRDAHCNDPTYQMFG

SSAFDDDDHQPLDSFAMELSGPR (SEQ ID NO: 59)

*Arabidopsis thaliana* RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 tttaaaaaccttgctagttctcaattctcatgactttgcttttagtctttagaagtggaaa  
 ATGGAAACATGGATCATCCCGTGGCTTTATTGGCTGATTCTATTTCGATTTTGTTC  
 AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA  
 GGTGACCATACAACAATAATACTCCAAGCTGGAATGCCACTCAGTTTACTCCATGTTCA  
 TGGTTTCATGTTACTTGCAATACTGAAACAGTGTACTCGTCTTGACCTGGGAGTGCT
- 15 AATCTATCTGGAGAACTGGTGGCCAGCTTGCTCAGCTCCAAATTGCAGTACTTGAA  
 CTTTTTAAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGGCGACTGTATGGA  
 GTAAGCTTGGACCTTTTGGCAAAACATAAGCGTCCCATCCCTCTCTTGCCAAA  
 CTAGGAAAACCTCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATCCAGG  
 TCTTTGACTGCTCTGCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT
- 20 ATTCTGTTAATGGTTCTTTTCGAGTTCACCTCTATGAGTTTGCCAATAATAAATTA  
 AGGCCGCGACCTGCATCTCCTTCACCATCACTTCAGGAACGCTCGCAGCAATAGTAGT  
 GGAGTTGCTCGGGTGCAGCACTTCTATTGCGCTTGCTTGGTGGCTGAGAAGAAAAC  
 CAGGGTCACTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGTTTATTAGACAATTT  
 AAAAGGTTCTCCTTGCGTGAACCTGCTAGTTGCTACAGAGAAATTAGCAAAAGAAATGA
- 25 TTGGGCAAGGACGTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGT  
 GCTGTGAAACGGCTAAATGAAGAAGTACCAAGGTGGGGAACCTGCAGTTTCAAACCGAA  
 GTTGAGATGATCAGTATGGCCGTTCTAGGAACCTTGCTTCGCTCTGCTGCTTTGCTG  
 ACTCCAACCTGAAAGATTACTTGGTTTATCCCTACATGGCTAATGGAAGTGTGCTTCTTGT  
 TTAAGAGAGCGTCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAGAAAGCATATTGCT
- 30 CTGGGATCAGCAAGGGGCTCGCATATTTACACGATCATTGOGAOCAAAAGATCATTCAC  
 CTGGATGTGAAGCTGCAAAATATACGTGTAGATGAAGAGTTTGAAGCTGTGTTGGAGAT  
 TTTGGGCTAGCAAAATTAATGAATATATAAGACTCCCATGTGACAACCTGCTGTACGGGT  
 ACGATTGGCCATATAGCGCCGAGTACCTCTCGACAGGAAATCTTCTGAGAAGACTGAT  
 GTTTTGGGTACGGGGTCTATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTCGATCTT
- 35 GCTCGGCTTGCAAAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTGA  
 GAGAAGAGTTGAAAGCCTTGTGGATGCAGAACTGGAAGGAAAGTACGTGGAACAGAA  
 GTGGAGCAGCTGATACAAATGGCTCTGCTCTCACTCAAAGTTCTGCAATGGAAGCTCCA  
 AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTAGCTGAGAGATGGGAAGAA  
 TGGCAAAAGGAGGAGATGCCAATACATGATTTTAATCTCAAGCCTATCCTCATGTGCG
- 40 ACTGACTGGCTCATCCCTATTCCAATTCCCTTATCGAAAAGGATTACCCCTCGGGGCCA

AGATAAACccttttagaaagggtcatttcttgggttcttcaacaagtatatataggtgta  
gtgaagttgtaagaagcaaaacccacattcaccttgaatatcactactctataa (SEQ ID NO: 60)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS12 protein.

Different domains are spaced and shown from the N-terminus  
10 towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 2 leucine residues, each  
15 separated by seven other amino acids. The third domain  
contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
20 contains many serine and proline residues, and is likely to  
contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
25 function. The eight domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
30 leucine rich repeat, probably involved in protein / protein  
interactions.

MEHGSSRGFI  
WLILFLDFVSRVTGKTQV

35

DALIALRSSLSGGDHTNNILQ  
SWNATHVT

PCSWFHTCNTENSVTRL

DLGSANLSGELV

P QLAQLPNLQYLELFNNITGEI

5 PEELGDLMEVSLDLFANNISGPI  
PSSLGKLGKLRFLRLYNNLSGSI  
PRSLTALP LDVLDISNNRLSGDI  
PVNGSFSQFTSMRFA NNKLRPR

10 PASPSPSPSGGTS

AAIVVGVAAGALLFALAWWL

RRKLQGHFLDVPAAEEDPE

15 VYLGQFKRFSLRELLVAT

EKFSKRNVLGKGRFGILYKGRLLAD

DTLVAVKRLNEERTKGGELQFQ

TEVEMISMAVHRNLLRLRGFCM

20 TPTERLLVYPYMANGSVASCLR

ERPEGNPALDWPKRKRIALGSA

RGLAYLHDHCDQKIIHLDVKAA

NILLDEEFVAVVGFGLAKLMN

YNDSHVTTAVRGTIHIAPEYL

25 STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKLES LVD AELEGY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVVRMLE

30

GDGLAERWEEWQKEEMPIRDFNYQAY

PHAGTDWLI PYSNLIENDYPSGPR (SEQ ID NO: 61)

35

*Arabidopsis thaliana* RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctastaataatggctttgcttttactctgatgacaagttcaaaaATGGAA  
 10 CAAAGATCACTCCCTTTGCTTCCCTTATCTGCTCCTACTATTCAATTCACCTCTCAGAGTC  
 GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTCATCAGGTGAC  
 CCTGCAAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTTACTCCATGTACTTGGTTT  
 CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTGACCTTGGGAATGC AAAACTA  
 TCTGGAAAGTTGGTCCGAACCTTGGTCAGCTTTTAAACTTCGAGTACTTGGAGCTTTAT  
 15 AGCAATAACAATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGGAACTAGTAAGC  
 TTGGATCTTTACGCAAAACAGCATAAGCGGTCCCATCCCTTCGCTCTCTTGGCAACTAGGA  
 AAACCTCCGGTCTTGCGCTTTAACACAATAGCTTATCAGGGGAAATTC CAATGACTTTG  
 ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAAACAATCGGCTCAGTGGAGATATTCCT  
 GTTAATGGTTCTTTTTCGCTCTTCACTCCTATCAGTTTTCGGAATAATAGCTTAACGGAT  
 20 CTTCGCCGAACCTCCGCTACTTCTACTCTCCTACGCCACCACACCTTCAGGGGGGC AA  
 ATGACTGCAGCAATAGCAGGGGGAGTTGCTGCAGGTGCAGCACTTCTATTTGCTGTTCCA  
 GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAAAC CAGGACCACTTTTTTGATGTACCT  
 GCTGAAGAAGACCCAGAGGTTCAATTAGGACAACCTCAAAGGTTTACCTTGCCTGAAC TG  
 TTAGTTGCTACTGATACTTTAGCAATAAAATGTAITGGGTAGAGGTGGTTTGGTAA A  
 25 GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAA AAGAAGAA  
 CGTACCAGAGGTGGGGAAC TGCACTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT  
 CATAGGAAC TTGCTCGGCTTCGTGGCTTTTGATGACTCCAAC TGAAGATTACTTGTGT  
 TATCCCTACATGGCTAATGAAGTGTTGCTTCTGTGTTAAGAGAGCGTCTGAAGGCAAT  
 CCAGCACTTGATTGGCCAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGGG  
 30 TATTTACATGATCATTGCGACAAAAAATCATTACCGGGATGTTAAAGCTGCTAATATA  
 TTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT  
 TATAATGACTCCCATGTGACAAC TGCTGACGCGTACAATTTGGCCATATAGCGCCCGAG  
 TACCTCTCGCAGGAAATCTTCTGAGAGACTGATGTTT TGGGTACGGGGTCATGCTT  
 CTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTTCTCGGCTTGCAAAATGATGATGAT  
 35 ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAGCCTTGTG  
 GATGCAGAACTCGAAGGAAGTACGTGGAAACAGAAAGTGAGCAGCTGATACAAATGGCT  
 CTGCTCTGCAC TCAAAGTTCTGCAATGGAACGTCCAAGATGTCAGAAGTAGTGAGAATG  
 CTGGAAGGAGATGGTTAGCTGAGAGATGGGAAGATGGCAAAAGGAGAGATGCCAATA  
 CATGATTTTAACTATCAAGCCTATCCTCATGCTGCACTGACTGGCTCATCCCTATTTCC  
 40 AATTCCTTATCGAAAAAGATTACCCCTCGGGTCCAAGATAAccttttagaagggtcctt



ttcttgtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa  
aa (SEQ ID NO: 62)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS13 protein.

Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
described in Schmidt et al. (1997).

10

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains  
leucine zipper motifs, containing 2 times 2 leucine residues,  
each separated by seven other amino acids. The third domain  
contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
contains many serine and proline residues, and is likely to  
contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
function. The eighth domain represents a serine / threonine  
protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
leucine rich repeat, probably involved in protein / protein  
interactions.

30

MEQRSLLCFLYLL  
LLFNFTLRVAGNAEG

35

DALTQLKNSLSSGDP  
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV  
P ELGQLLNLYLELYSNITGEI  
PEELGDLVELVSLDYANSISGPI  
5 PSSLGKLGKIRFLRLNNSLSGEI  
PMTLTSVQLQV LDISNNRLSGDI  
PVNGSFSLFTPISFANNSLTDLPE  
  
PPPTSTSTPTPPPSG  
10 GQMTAAIAGGVAAGAAL  
LFAVPAIAFAWWL  
  
RRKPQDHFFDVFGEEDPE  
15 VHLGQLKRFTLRELLVAT  
  
DNFSNKNVLGRGGFGKVYKGRGLAD  
GNLVAVKRLKEERTKGGEIQFQ  
TEVEMISMAVHRNLLRLRGFCM  
20 TPTERLLVYPYMANGSVASCLR  
ERPEGNPALDWPKRKHIALGSA  
RGLAYLHDHCDQKTIHRDVKAA  
NILLEDEFEAVVGDFGLAKLMN  
YNDSHVITAVRGTIIGHIAPEYL  
25 STGKSSEKTDVFGYGVMLLELI  
TGQKAFDLARLNDDDIMLLDW  
VKEVLKEKKLESVDAELEGKY  
VETEVEQLIQHALLCTQSSAME  
RPKMSEVVVRMLE  
30 GDGLAERWEEWQKEEMPIHDFNYQA  
  
YPHAGTDWLIIPYSNLIENDYPSGPR (SEQ ID NO: 63)  
35

*Arabidopsis thaliana* RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 ctgcaccttagagattaataactctcaagaaaaacaagttttgattcggacaaag**ATGTTG**  
CAAGGAAGAAGAGAAGCAAAAAAGAGTTATGCTTTGTTCTCTTCAACTTCTTCTTCTC  
TTTATCTGTTTCTTCTTCTTCTTCTGCGAACTCACAGACAAAGTTGGTGCCTTAATA  
GGAACTCAAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATGGGATGACACAGCA  
GTTGATCCATGTAGCTGGAACATGATCACTTGTCTGATGGTTTGTCAATAGGCCTAGAA  
15 GCTCCAAGCCAAACTTATCAGGAACCTTTTCATCAAGTATTGGAATTTAACAATCTT  
CAAACTGTATACAGGTTATTGCAGAACATTTACATAACAGGAAACATCCCTCATGAGATT  
GGGAAATTGATGAACTCAAAACACTTGATCTCTTACCAATAACTTCACCTGGTCAAATC  
CCATTCACCTCTTTCTACTCCAAAAATCTTCACAGAGGGTTAATAATAACAGCCGTGACA  
CGACAAATTCCTAGCTCATTTGGCAACATGACCCAACTCACTTTTGGATTGTGCTCAT  
20 AATAAATTGAGTGGACCAAGTTCCAAGATCACTTGCCAAAAATTCATGTTATGGGCAAT  
TCTCAGATTGTCCAACAGGAAGTGAAGAGCTGTAATGGGACTCAGCCTAAGCCAAATG  
TCAATCACCTTGAAACAGTTCTCAAGAACTAAAAACCGGAAATCGCGGTAGTCTTCGGT  
GTAAGCTTGACATGTGTTGCTTGTGATCATTTGGCTTTGGTTTCTCTTTGGTGGAGA  
AGAAGACATAACAAACAAGTATTATCTTTGACATTATGAGCAAAACAAGGAAGAAATG  
25 TGCTAGGGAATCTAAGGAGGTTTAATTTCAAAGAAGCTTCAATCCGCACTAGTAACCTC  
AGCAGCAAGAATCTGTCGGGAAAGGAGGGTTTGGAATGTGTATAAAGGTTGTCTTCAT  
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT  
GATTTTCAGACAGAGCTTGAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA  
TAGCGTTCTGTACTACTTCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAAATGGC  
30 AGTGTGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGCACAGAAGCGAATA  
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTGATGAGCAATGTGATCCAAGATCATT  
CACCTGTATGTCAAAGCTGCGAACAATACTTCTTGACGATTACTTTGAAGCTGTTGTGCGA  
GATTTGGGTTGGCTAAGCTTTGGATCATGAGGAGTCGATGTGACAAACCGCGTGAAGA  
GGAAACAGTGGGTACATTGCACTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA  
35 GATGTGTTGGTTTCGGGATTCTTCTTCGAATTGATTACTGGATTGAGAGCTCTTGAA  
TTCGGAAAGCAGCAAAACCAAGAGGAGCGATCTGATTGGGTAAGAACTACACAACA  
GAGAAGAGCTAGAACAGATAGTAGACAAGGATTGAAGAGCAACTACGATAGATAGAA  
GTGGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCATTACCGTCT  
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGCGATGGTCTGTTGAGAATGGGAGCT  
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAACCTAACGAGTTTCTTCTCTT

GAACGTTATTTCGGATCTTACAGATGATTCTCGGTGCTGGTTCAGCCATGGAGTTATCA  
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa (SEQ ID NO: 64)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*  
RKS14 protein.

Different domains are spaced and shown from the N-terminus  
towards the C-terminus. Overall domain structure is similar as  
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain  
represents a signal sequence. The second domain contains a  
leucine zipper motif, containing 3 leucine residues, each  
separated by seven other amino acids. The third domain  
15 contains conserved cysteine residues, involved in disulphate  
bridge formation. The fourth domain contains a leucine rich  
repeat domain, consisting of 5 complete repeats of each  
approximately 24 amino acid residues. The fifth domain  
contains many serine and proline residues, and is likely to  
20 contain hydroxy-proline residues, and to be a site for O-  
glycosylation. The sixth domain contains a single  
transmembrane domain after which the predicted intracellular  
domains are positioned. The seventh domain has an unknown  
function. The eight domain represents a serine / threonine  
25 protein kinase domain (Schmidt et al. 1997) and is probably  
also containing sequences for protein / protein interactions.  
The ninth domain has an unknown function. The last and tenth  
domain at the C-terminal end represents part of a single  
leucine rich repeat, probably involved in protein / protein  
30 interactions.

MLQGRREAKKSYALFSSTFF  
EFFICFLSSSAELTDKV

35 VALIGIKSSLTDP  
RGVLMNWDDTAVD

PCSWNMITCSDFVIR

LEAPSQNLSGTLSS  
SIGNLTNLQTVYRLQNNYITGNI  
PHEIGKLMKLTLDLSTNNFTQOI  
5 PFTLSYSKNLHRRV NNNSLTGTI  
PSSLANMTQLTFLDLSYNNLSGPV  
PRSLAKTFNVMGNSQICPT  
  
GTEKDCNGTQPKMSITLNSSQR  
10 TKNRK  
  
IAVVEGVS LTCVCLLIIGFGFLLWW  
  
RRRHNKQVLFFDINEQNKE  
15 EMCLGNLRRFNFKELOSAT  
  
SNFSSKNLVGKGGFNGVYKGCLHD  
GSI IAVKRLKDINNGGGEVQFQ  
TELEMISLAVHRNLLRLYGFT  
20 TSSERLLVYPMSNGSVA  
SRLKAKPVLWDGTRKRIALGAG  
RGLLYLHEQC DPKIHRDVKAA  
NILLDDYFEAVVGDFGLAKLLO  
HEESHVTTAVRGTVGHIAPEYL  
25 STGQSSEKTDVFGFGILLLELI  
TGLRALEFGKAANQRGAILDW  
VKKLQQEKLEQIVDKDLKSNY  
DRIEVEEMVQVALLCTQYLPFH  
RPKMSEVVRMLE  
30 GDGLVEKWEASSQRAET  
NRSYSKPNFESS  
  
ERYSDLTDDSSVLVQAMELSGPR (SEQ ID NO: 65)  
35

## Legends

Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

- The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

- 35 Alignment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

- 5 Intron-Exon boundaries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

- 15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

- Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects.
- 20
- 25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

- 30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.
- 35

## Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

## Figure 9

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

## Figure 10

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared



with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GASA3 gene in sense direction, i.e. overexpressing GASA3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

- 10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
- 15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
- 20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25 Figure 12

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense

30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified ). Epidermal cell size is not changed in transgenic plants compared with the control.

10

## Figure 14

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermis of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

## 20 Figure 15

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct. The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

## 30 Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

35

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (s)

5 Figure 17

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 Figure 19

Seedlings from *transgenic Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

## Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

## Figure 24

Average root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

## Figure 25

T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

## Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from transgenic RKS and ELS transgenic roots.

## Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken under same magnification.

## Figure 28

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems.

The generative shoots are photographed with similar magnification.

Figure 29

*Arabidopsis thaliana* WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

#### Figure 32

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be observed.

#### Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

10 Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.



## Detailed description

## 1. Modifying organ size

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

30

the size of plant organs  
the growth rate  
the yield of harvested crop  
the yield of total plant material  
the total plant size

35

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:  
the size of plant organs

the growth rate  
the total plant size

5

**Results obtained (see also figures 6 to 13)**

Overexpression and antisense constructs of full length RKS  
cDNA clones have been made under the control of 35S  
promoters. Transgenic plants have been produced in *Arabidopsis*  
10 *thaliana* and in *Nicotiana tabacum*. Subsequent generations of  
stably transformed plants were investigated for phenotypes and  
analyzed in detail. The phenotype observed in transgenic  
plants with antisense constructs of RKS4 (GT-RKS4-a) could be  
described as dwarf plants in which all plant organs showed a  
15 decrease in organs size and growth rate. Overexpression of  
RKS4 (GT-RKS4-s) resulted in plants with increased size of  
organs and an increase in growth rate. Since cell size alone  
was not responsible for the modifications in organ size of  
petals it can be concluded that RKS4 is involved in the  
20 regulation of the cellular divisions during plant growth and  
organ formation. Overexpression of RKS 4 results in an  
increase of cellular divisions whereas a decrease in  
endogenous RKS 4 gene product levels within the plant results  
in a decrease of cellular division rates.

25

**Literature**

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30 *Arabidopsis*. P.M Donnelly et al. 1999; Developmental biology  
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## 2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

### 30 Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:

- the size of plant organs
- the growth rate
- 35 the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS signaling complex members in order to decrease:  
the size of plant organs

- 5 the growth rate  
the total plant size

#### Results obtained

- Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division. Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10
- 20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding
- 25 cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants, no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within
- 30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.
- Normal RKS10 function also involves an activation process on
- 35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

15

#### Literature

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### 3. Regeneration

- Modification the levels of different RKS and ELS genes within
- 5 plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and
- 10 IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. herewith the invention provides a method for modulating a developmental pathway of a plant or plant
- 15 cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular
- 20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction.
- 25 Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the
- 30 corresponding expression cassettes in the plant genome.

### Results obtained

- Overexpression and antisense constructs of full length RKS and ELS cDNA clones have been made under the control of 35S
- 35 promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

#### Literature

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- 10

#### 4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

#### Results obtained

- 5 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector (pGreen5K) were tested for their ability to induce fasciation (Overexpression constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in
- 15 fasciated plants, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only positive results are shown). Antisense constructs of RKS3 gave also rise to fasciation (Figure 19).

20

#### Literature

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- 25 loop regulated by CLV3 activity.
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## 5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

- hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or
- 5 ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be
- 10 influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

#### Results obtained

- 15 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 20 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root
- 25 development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown
- 30 together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

35

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## 6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly be seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

### Results obtained

Changing the normal levels of endogenous RKS10 within the plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28). Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places where normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic



developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show

5 the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the

10 meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded

15 from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together

20 with other phenotypes (results not shown).

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## 7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5' end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3' end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

### 30 Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

25

### Literature

- The *Arabidopsis* male sterility1 (MS1) gene is a transcriptional regulator of male gametogenesis, with homology to the PHD-finger family of transcription factors. Wilson et al. 2001. the Plant Journal 28: 27-39
- Transposon tagging of a male sterility gene in *Arabidopsis*. Aarts et al. 1993. Nature 363: 715-717

35

## 8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the

- 5 SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling
- 10 complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

- 15 **At2g27080;**  
MAERVVPADS PPQSGQFSGN PSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ  
LSRKKTNRSN CRCCFCSFLA AVFILIVLAG ISFAVLILIY RPEAPKYSIE GFSVSGINLN  
STSPISPSFN VTVRSRNGNG KIGVYYEKES SVDVYYNDVD ISNGVMPVYF QPAQNTVTVK  
LVLSGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWIMI VNVDCDVTVD  
20 KLTAPSRIVS RKCSHDVDLN \*\* (SEQ ID NO: 66)
- At5g21130**  
MTVEKPEQMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSES RYSVDSQKSR IGPPPGTTVI  
KLPKDQIYRV PPPENAHRYE YLSRRKTNKS  
25 CCRCLCYSL SALLIIIVLA ALAFGFFYLV  
YQPHKPFQSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGILIYKQ NEADVFFNGT  
KLNGEFTAF KQPAGNVTVI VTVLKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF  
KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL L\* (SEQ ID NO: 67)
- 30 **At1g65690**  
MSQHQKIYPV QDPEAATARP TAPLVRGSS RSEHGDPKSV PLNQRPQRFV PLAPPKYGRS  
CCRCFCYCTP CFLLLLVAIV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTFAT  
NVTITAKNPN EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI VVMTGTQTN  
ASGLRTTLEE QQQTQNTIPL RIRVNGQVVRV KFGKLKLFV RFLVRCGVFV DSLATNNVIK  
35 IQSSSCKFRLL RL\* (SEQ ID NO: 68)
- At5g36970**  
MSDBQKIHPV SDPEAPPHT APLVPRGSSR SEHGDPKTYQ QAPLDPFRE KKGSR  
CWCRVCYCTLLVLF LLIVIVGAIV GILXIVFRPK FFDYNIDRLQ LTRFQINQDL  
40 SLSTAFNVTI  
MTKIPNEKIG IYYEDGSKIS VLYNQTRISN GSLPKFYQGH ENTITILVEM TGFTQNTSL  
NTTLQEQQLL TGSIFLRIRV TQPVRIKLG LKLMKVRFLV RCGVSVDSLA ANSVIRVRS  
NCKYRFL\* (SEQ ID NO: 69)
- 45 **At1g54540**  
MGDQKIHVP LQMEANKTKT TTPAPGKVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL  
LVIALIALAI AVAVVYFVPH PKLPSEYVNS LRVNLGINL DLSLSAEFKV EITARNPNK  
IGIYYEKGH IGVWYDKTKL CBGPPIRFYQ GHRNVTIKLV ALTGRAQYGN TVLAALQQOQ  
QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL TNNNNINIK SDCSPKAKL\* (SEQ ID NO: 70)
- 50 **At5g06320**

- MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLGG  
IAALILWLIF RPAIAKFVVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYDEIE  
VSGYGGQDRF GMSNNISKPY QGHKNTTVVG TKLVGQQVLV LDGGERKDIN EDVNSQIVRI  
DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PITSNSTSGF VFQPTKCDVD P\*\* (SEQ ID NO: 71)
- 5 At5g11890  
MTDRVFPASK PPTATNGAPP VGSIPPPAP ATVTSNGTIN GMANQKPQVY IPANRPVYRP  
QPYRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSPVPSI  
RISRVNLTTT SDGSSVSHLS FNFPTLISEN PHQHLSPSYD PFTVTNSAK SGTMLNGTV  
10 PAFPSDNGNK TSFHGVIATS TAARELDPDE AKHLRSLDTR ARVGYEIMR TKVXIMGKL  
KSEGVRIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLVS KVMKMF\* (SEQ ID NO: 72)
- At1g17620  
MTDRVYPAS KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG  
15 CCCRCCCTWIFVII LLLLVAAAA AVVYLIYRQP RPSFTVSELK ISTLNFTSAV  
RLTTAISLSV  
IARNPNKRVG FIYDVTDITL YKASTGGDDD VVIGKGTIAA FSHGKNITT LRSTIGSPPD  
ELDRISAGKL KGLKAKKAV AIKIVLNSKV KVMGALIKTP KSGIRVTCBG IKRVAPTQKK  
ATTATTSAAK CKVDPRFKIW KITF\*\* (SEQ ID NO: 73)
- 20 At3g11650  
MGSKQPYLNG AYYGPSIPP PKAHRSYNSP GFGCCCCFCL GSCLCRCCGC ILSLICNILI  
AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDNN NLHYSLDLNF TIRNPNQVGV  
25 VYVDEFSVSG YYGQDRFGSA NVSSFYQGHK NTTVILTICE QONLVVLGDG ARTDLKDEK  
SGIYRINAKL RLSVRPKFWF IKSXKLKPKI KCDDLKIPLG SSNSTGGFKP QPVQCDFLS\*\* (SEQ ID NO: 74)
- At2g22180  
MEGRRRPPSA TAPDSDDDKP DDPSPVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL  
30 PTTSSPPLRP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPK NKKKGCCSKRL  
LWFFILLVIF GFLLGAILLI LHFAPNPTLP VFAVERLTVN PSNFVETLRA ENPTSNMGVR  
YNMEKGVVVS LTYKNKSLGS GKFPGLSQAA SGGDKVNVKL NGSTKNAVQ PRGSKQPVVL  
MLNMEKAEY RAGPVKRNKE VVVTCDVKVK GLLDAAKVEI VSENCSEFK N\* (SEQ ID NO: 75)
- 35 At5g22870  
MCHKPKLELM PMETSPAQPL RRPSLICYIF LVILTLIPMA AVGFLITWLE TKPKKLRYTV  
ENASVQNPNL TNDNHSATP QFTIQSHWPN HRISVYYSV EIFVKPDQT LAFDVTBPFH  
QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFKARVRFK VGIWKSHER  
AKIKCSHTV SLSQPNKSQN SSCDADI\* (SEQ ID NO: 76)
- 40 At2g35980  
MAAQPLNGA FYGPSVPPPA PKGYRRRGH RGCOCCLLSL FVKVILSLIV ILGVAALIFW  
LIVRPRAIKF HVTDASLTRF DHTSPDNLIR YNLALTVPVR NPNKRIGLYY DRLEAHAYE  
GRRFSTITLT PFYQGHKNTT VLTPPTQSQN LVIFNAGQSR TLNAERISGV YNIBIKFLRL  
45 VRFLGDLKLF RRIKPKVDCD DLRLPLTSTN GTTTTSTVFP IKCDFDF\*\* (SEQ ID NO: 77)
- At2g46300  
MADYQMNPLV QKPPGYRDPN MSSPPPPPPP IQQQPMKRAV PMPTSYRPFK KRRSCCRFC  
CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLASFRLD GFKLADDDPG ASLSATAVAR  
50 VEMKNPNKSL VFYIGNTAVD LSVGSGNDET MGGETTMNGF RQGPKNSTSV XVTFTVQNL  
VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCCGVVS LNKLTDSPK  
CILNTLKMYK IISN\* (SEQ ID NO: 78)
- At4g05220  
55 MTPDRTTIPI RTPVPVRAQP MKRHHSASY AHRVRESLST RISKFICAMF  
LVLVLFVGV I AFILWLSLRP HRPRFHIQDF

- VVQGLEDQPTG VENARIAFNV TILNPNQHMVG VYFDSMEGSI YYKDQRVGLI  
 PLLNPFVQQP TNTTIVTGTI TGASLTVNSN RWTFSNDRA QGTVGFRLDI  
 VSTIRPKLHR WISKHRMHA NCNIVVGRDG LILPKFNHXR CPVYFT\* (SEQ ID NO: 79)
- 5 At2g35460  
 MANGLGASGY GPPIKPPVKT YYSHGRGSD VGCGICGCF SCLLCCGGCL VNIICNILIG  
 VLVLGGVVAL ILWFILRPNV VKFQVTEADL TRFEPDRSH NLHYNISLNF SIRPNQRLG  
 IHYDQLEVRG YYGQDRPSAA NMTSFYQGHK NTVVGTGLN GQKLVLGAG GRDRFREDRR  
 SGVVRIDVKL RFLKRFKFG LMSWAVERPKI KCHLVFLST SSSDERFQFH PTKCHVDL\* (SEQ ID NO: 80)
- 10 At2g27260  
 MQDPSRPATG YPYFYPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYP QPNPRAVIIR  
 RLFIVTFTFL LLLGLILFIF FLIVRPQLPD VMLNSLSVSN FVSNNOVSG KWDQLQFRN  
 PMSKMSLHYE TALCAMPYNR VSLSETRLOP FDQGGKQDTV VKNATLSVST YVDGLRVD SI  
 15 GKERSVKGNV EFDLRMISYV TPRYGAFRRR RYVTVKCDVD AVGVPSVSGE GRMVGSSKRC  
 KTY\*\* (SEQ ID NO: 81)
- At4g01410  
 MGEGBAKAEH AAKADHKNP SASSTPESY KEGGGGGGA RRAICGAFT ILVILGIAL  
 20 ILMLVYRPHK PRLTVVGAARI YDLNFTAPPL ISTSVQFSL ARNPNRRVSI HYDKLSMYVT  
 YKQIITPPL PLPPLRLGHK STVVIAPVMG NGIPVSPV ANGKND EAY GVVLHRVIF  
 GRLEWKAAGI KTGRYGFYAR CDVWLRNFP SNGQVLLAP STCKVDV\* (SEQ ID NO: 82)
- At5g22200  
 25 NTGRYCDQHN GYBERRMRM MRRIANACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTI  
 MDPNVQPNF LSSNLQVTS SRNPNDKIGI FYDELDTVT YRNQSVTLAR LLPSTYQGH  
 EFTWSPFLI GSAVPVAPYL SSALNEDFLA GLVLLNIKD GWVRWKVGSV VSGSTRLEVN  
 CFAFITVTGK LTGTGPAIKY QLVQRCAVDV\* (SEQ ID NO: 83)
- 30 At1g61760  
 MENKVDLSLV RSNPSTRPIS RHHSASHNV RVKESLTTVR SKLICAIFLS LLLCLGIITF  
 ILWISLQPHV PRVHIRGFISI SGLSRPDGFE TSHISFKITA HNPQNVOGIY YDSMEGSVYI  
 KEKRIGSTKL TNPFYQDPKN TSSIDGALS PAMAVNKNRM MEMERDRNQ MEMERLKVRS  
 MIRPKVYTWK SKSHMYASC YIEIGWDGML LSATDKRCP VYFT\* (SEQ ID NO: 84)
- 35 At3g52470  
 MSKDCGNHGG GKEVVVRKLC AAIAPFIV LITIFLVWVI LRPTKRFVL QDATVYAFNL  
 SQPHLLTSNF QVTIASRNFN SKIGIYDRL HVYATYMNQ ITLRTAIPPT YQGHKEVIVW  
 SFPYGTAVP IAPYNSVALG EKKDRGFVGL MIRADGTVRN KVRTLITGKY HIHVRCAFI  
 40 NLGKKAAGVL VGDHAVKYTL ANKCSVWV\*\* (SEQ ID NO: 85)
- At5g53730  
 MSQISLTSPP HCAKKGGINI NNREKKLFPT FSTFFSGLLL IIFLVMLILH PERPEFSLTE  
 ADIYISNLTT SSTHLLNSSV QLTLFSKNFN KKGVIYDKL LVYAAYRGQQ ITLSEASLQ  
 45 YQSHEEINLL TAFLLQGTLP VAQSFYQIS RERSTGKII QMKMDGKLW KIGTWVSGAY  
 RFNVNCLAIV AFGNMNMTTP LASLQGTCS TTI\* (SEQ ID NO: 86)
- At4g01110  
 MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSMLNR PPKHAIPAAF YPTKKRQWSR  
 50 CRVFCVVCI TVAVILLILI LTVSVFPLYI SPRLPVRLS SFRVSNFNS GGKAGDGLSQ  
 LTAEATARLD FRNPNGLKRY YGNDVDVVS VOEDDEFTSL GSTKVKGFB KPGNRTVVIV  
 PIKVKQQVD DPTVKRLRAD MKSKLVVKV MAKTVKVGV GRKIVTVGV TISCGVRLQ  
 TDSKMSKCT IKMLKWYVPI QVKCI\* (SEQ ID NO: 87)
- 55 At2g35960  
 MTKDCGNHG GGGGGGTASR ICGVIIGFII IVLTTIFLVW IILQPTKPRF ILQDATVYAF



NLSQPNLLTS NFQITIASRN RNSRIGIYD RLHVYATYRN QQITLRTAIP PTYQGHKEDN  
VMSPPFYVGNV VPIAPFNAVA LGDEQNNGFV TLIIRADGRV RWKVGTLTITG KYHLHVRCAQ  
FINLADKAAG VEVGENAVKY MLINKCSNV \* (SEQ ID NO: 88)

## 5 At3g52460

MPSPPEEBETQ PKPDTPGQON SERDINQPPP PPQSQPPPPP QTQQTTPPV MGYPGYHQP  
PPYNYPNAP YQYYPYAQAP PASYYGSSYP AQONPVYQRP ASSGFVRGIF TGLIVLVVLL  
CISTTITWLW LRPQIPLFSV NNFVSNSFNW TGPVFSAQWT ANLTENQNT KLGKGYFDRIQ  
GLVYHQNAVQ EDEPLATAFF QPVFVETKKS VVIGETLTAG DKRQPKVPSW VDEBMKKERE

10 TGTVTPLSLRM AWWVTPKTDG WAARESSGLKV FCGKLKVGFE GLSGNGAVLL PKPLPCVVYV\* (SEQ ID NO: 89)

## At4g09590

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV WIILOPKNPS FILQDITVYA  
FNLQSNLLT SKFQITIASR NNSNIGIYY DHLHAYASYR NQOITLASDL PPTYQRHKED  
15 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTITLI GNYHLHVRCAQ  
AFINQADKAA GVHVGENTVK YTLINKCSVN F\* (SEQ ID NO: 90)

## At2g35970

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPS FILQDITVYA  
FNLQSNLLT SKFQITIASR NNSNIGIYY DHLHAYASYR NQOITLASDL PPTYQRHKED  
20 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTITLI GNYHLHVRCAQ  
AFINQADKAA GVHVGENTVK YTLINKCSVN F\* (SEQ ID NO: 91)

## At3g26350

MSHHHHHETN PHFARIPSQN PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHFVA  
PGLILKTRG RHRENPIQEP KHSVIPVPLS PEERLPPRKT QNSSKRPLLL SPEDNQQRFP  
PPQQAQRNG GGYGSTLPPI PKPSFWRTAP TSPHRRRGP RLPPPSRETN AMTWSAAPCC  
15 ALFWLILILG GLILILVYLV YRPRSPYVDI SAANLNAALY DMGFLNLGDL TILANVTNPS  
KSSSVFESYV TFEIYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRRELQR

30 QETGTPVLLN LRGMFHARSH IGPLFRYSYK LETHCSVSLN GPPLGAMRAR RCNTRK\* (SEQ ID NO: 92)

## At3g11660

MKDCEHHGHS RRKLIRRIWF SIIFVLFIF LTIILLIWAII QPSKPRFILQ DATVYAFNVS  
GNPPNLLTSN PQITLSSRN NKGIGIYDR LDVYATYRSQ QITPPTSIPP TYQGHKVDI  
35 WSPFVYGTSV PIAPFNGVSL DTDKNGVVL LIIRADGRVW WKVGTFTIGK YHLHVKCPAY  
INFGNKAQV IVGDNAVXYT FTTSCSVSV\*\* (SEQ ID NO: 93)

## At3g44220

MTEKECEHHH DEDEKMRKRI GALVLGLAA VLFVVFLVWA ILHPHGPRFV  
15 LQDATIYAFN VSQPNYLTSN LQVTLSRRNP NDKIGIFYDR LDIYASYRNP  
QVTIALLLPA TYQGHLDVTI WSPFLYGTTV PVAPYFSPAL SQDLTAGMVL  
LNKIDGWVR WKVGTWVSGR YRLHVNCAPY ITLAGHFSGD GPVAKYQLVQ RCAVDV\* (SEQ ID NO: 94)

## At1g08160

MVPFNFAHQ ARRTQPQLQP QSQPRAQPLP GRMMNPVLCI IVALVLLGLL VGLAILITYL  
15 TLRPKLLIYT VEAASVQEFA IGNNDDHINA KPSYVIKSYN PEKHVSVRHY SMRISTAHNN  
QSAHKNISP PKQRPNKETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS  
YKTWIFRSRR RTLKAVCTFV MINVTSSSLD GPQRVLCKTR L\*\* (SEQ ID NO: 95)

## 50 At2g01080

MPPPPSSSRA GLNGDFIAAQ NQQPYYSYS SSSSASLKGC CCCLFLLFAF LALLVLAVVL  
15 IYILAVFKKK PQFDLQVAV VYMGISNPSA VLDPTTASLS LTRIMLFTAV NPMKVGIRYG  
ESSFTVMYKG MPLGRATVPG FYQDAHSTKM VBATISVDVR NLMQAHADL VRDASLNDVR  
LNLTRVDGYGA KIRVMNFDSP GVQVLLPSFL PAFCSLSDLA \* (SEQ ID NO: 96)

55

## At5g05330

- MTSKDCGSHD SHSSCNRKIV INTISIILL ILVWILLVMA ILQPSKPRFV LQDATVPFNFN  
VSGNPPNLLT SNFQFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSFM LTTYQGHKEV  
NVWSPFVGGY SVPVAPYNAP YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLVHRCH  
ALINFQSSAA GVIVGKMYLT ETCSVSV\* (SEQ ID NO: 97)
- 5 **At5g56050**  
MSKFSPPQSS QPOPPETPPW ETPSSKWYSP IYTPWRTTTR STQSTPTPTT IALTEVIVSK  
SPLSNQKSPA TPKLDSMEAH PLHETMVLQ LRTSRTPWPI WCGAALCPIF SILLIVFGIA  
TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLQ LMFTNPNKKL NVRFENLMVE  
10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRROQT SNRIAYEIRS  
NFRVKALFGM IHSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW\* (SEQ ID NO: 98)
- At3g20600**  
NDRI  
15 MNQNEDETB GRNCTCCLS FIFTAGLTSL FLWLSLRADK PKCSIQNFFI PALGKDPNSR  
DRTTLNFMVR CDPNPKDKGI YDDVHLNFS TINTTKINSS ALALVGNVTV PKFYQGHKKK  
AKWGVQKPL NNQTVLRAVL PNGSAVFLD LKTOVRFKIV FWKTKRYGVE VGADVEVNGD  
GVKAQKKGIK MKKSDSSPPL RSSFFISVLM NLLVFFAIR\* (SEQ ID NO: 99)
- 20 **At3g54200**  
MSDFSIPKDD KKEEEKPATA MLPPPKPNAS SMBTQSANTG TAKKLRKRKN CKICICFTIL  
LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLOASVNP LLLKVLNLT LNVDLSLKNP  
NRIGFYDSS SALLNYRGQV IGEAPLPANR IAAKTKVPLN ITLTLMADR LSTQQLLSDV  
MAGVIPLMTF VKVTGKVTVL KIFKIKVQSS SSCDLSISVS DRNVTSHQCK YSTKL\* (SEQ ID NO: 100)
- 25 **At3g20590**  
non-race specific disease resistance protein, putative  
MTKIDPEEL GRKCTCFPK FIPTRLGAL ILWLSLRADK PKCSIQNFYI PALSKNLSSR  
DNTTLNFMVR CDPNPKDKGI YDDVHLTFS TINTTTTNS DLVLVANYTV PKFYQGHKKK  
30 AKWGVQVPL NNQTVLRAVL PNGSAVFLD LKTHVRFKIV FWKTKWYRI KVGADVEVNG  
DGVKAQKKGS KTKKSDSSLP LRSSFFIFVL MMLLVFFAIR\* (SEQ ID NO: 101)
- At4g39740**  
MSHVTATSLA RFTKFPVKPA SSPIVNTKLT TSGGRTAAFM DLSSFRLTVN  
35 DFDTANDSSG KFPWPRPLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT  
EMNNQMHRLE QKLLFLPLGS FLRLSTILH YPGECSNRPD PLEHALRRSR  
SLGLQDEEAA KKVIRVGRDS KNDVNVVFN QASFLRRCG PSKRIQSVNY  
CKSTROGHEI PDVKPLPFTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH  
VNDERRAVER GQASSNSGCG CGSNTTVKGP IIGGPTFLVS TENKIVTEND  
40 FCGKWVLLYF GYSFSPDVGP EQLKMMKSAV DKLAILNLNL TFGCLYLYAE  
FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVDT SHNMYLINPK  
MBIVRCFVGE YNFDLSQEL LKEVASVSQ\* (SEQ ID NO: 102)
- At1g32270 syntaxin, putative**  
MVRSDNVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR  
FEATVYYMNG RLGAVPMLPL YLGSKNTMLL RALFEGQTLV LLKGNERRKKF  
EDDQKTGVYR IDVKLSINFR VMVHLVLTWP MKPVVRCHLK IPLALGSSNS  
TGHHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA  
ALKEFQAKAH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QBQRVLMESR  
50 RQEIVLLDNE ISLNEARIEA REQIQEVKH QISEVMEMFK DLAVMVDHOG  
TIDDIDEKID NLRSAAGQK SHLVKASNTQ GSNSSLLFSC SLLFFFLSG  
DLRCRCVCGVS ENPRNLNPTTR KAWCEEDDEE GRKQKQKKKT MSEKRRRREK  
KVNKPNGFVF CVLGHK\* (SEQ ID NO: 103)
- 55 **At1g13050**

MSHHHYETNP HFVQFSLQDQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP  
 PETIHESFSS RPLFLRPEEP LPPRRNPNSA RPLQLSPPEQ RPPHRYGSE PTPWRRAPTR  
 PAYQQGPKRT KPMTLFATIC CAILLIVLIL SGLILLLVYL ANRPRSYPFD ISAATLNTAN  
 LDMGVVLNGD LAVVNVFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEFP IVPKGMMSMT  
 SFHLVSSQVQ IQMIQSQDLQ LQLGTGFVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL  
 NTPFAGTMRA RRCNTR\* (SEQ ID NO: 104)

**At5g45320**

MPRLTSRRGT SPFIWCAAI CAIISIVVIV GGIIVFVGYL VIHPRVPIIS  
 VADAHLDLFLK YDIVGVLTQ LTIIVRVEND NAKAHALFDE TEFKLSYEGK  
 PIAILKAPEF EVVKEKSMFL PYLVQSYPI LNPTMMQAVD YAVKKDVITF  
 ELKGGSRTRW RVGPLGSVKF ECNLSQCLRF RPSDHSYIPS PCTSAHKH\* (SEQ ID NO: 105)

**At3g20610**

MDRDDANEWF VTIVGSLMTL LYVSFLALCL LMLSTLVHII PRCSIHYFYI PALNKLSSIS  
 DNTLNFVNR LKNINAKQGI YYEDLHLSFS TRINNSLLV ANYTVPRFYQ GHEKKAKKVG  
 QALPFFNQTV IQAVLNGSA IFRVLDLMOV KYKVMWTK RYKLKASVNL EVNEDGATKV  
 KDEKDGIMKX ISDSFSQRLT FFQVCFSIIC VIMNWLIFLA IR\* (SEQ ID NO: 106)

**At4g26490**

MVLTKEATVR ENGLDAEPRK DRVILRQPRS SRTSLWICV AVFLAIRPRI PVFDIPNANL  
 HTIYFDTPEF FNGDLSMLVN FTNPNKIEV KFEKLRIELF FENRLIAAQ VQPFLLQKKE  
 TLEPIRLIS SLVGLPVNHA VELARQLENN KIEYERGTG KVKAHFGMIH YSYQLHGRGQ  
 LQMTGPPGTI LISRNCTTK \* (SEQ ID NO: 107)

**At5g42860**

MHAKTDESEVT SLASASPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV  
 LTPMGSGPPH SHSSSRFSK INGSKRKGHA GEKQFAMIEE EGLLDDGDRE  
 QEALPRRCYV LAFIVGFSLL FAFFSLILYA AAKPQKPKIS VKSITFEQLK  
 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSPP IDLSFSQITI  
 GSGIKKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK  
 KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLKGLVQPKF YKRIVCLINF  
 EHKKLSKHIP ITNNTVTISI \* (SEQ ID NO: 108)

**At1g45688**

MHAKTDESEVT SLAASSPARS PRRPVYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPHS  
 HSMGRHSRE SSSSRFSGSL KPGSRKNPN DGSKRKHGG EKQWKECAVI EEEGLDDGD  
 RDGGVPRCYV VLAFIVGFEI LFQFFSLILY GAAPKPKKI TVKSITFETL KIQAQDAGG  
 VGTDMITMNA LRMLYRNTGT TFFGVHVTST PIDLSFSQIK IGSGSVKKFY GQRKSERIVL  
 VHVIKEIPL YSGSGLTLLP APPAPLPKPK KKGAPVPIP DPPAPPAFV MTLSEFVRSR  
 AVVLGLVQFP KFYKIECDI NFEHKNLNKH IVITKNCTVT TV\* (SEQ ID NO: 109)

**At4g26820**

MDDEQNLVEE MNQQLITVI DTEKVPFLRP ISSRSHQSE PANISHWSLL FKLFLAITIM  
 GACVAGVTFF ILITPTPPTV HVQSMHISFA NNNLVPWSAT FSIKNPNEKL HVTYENPSVW  
 LVHRGKLVT ARADSEWQKG GEKNEVVKR NETKVIDEEA AWEMEDEVAV TGGVVLGDMV  
 FSGRVGFYPG TSALWGEQYM SAVCENVSAT LYNVDDEIYG TNRSVLSDFG RLVCVSRLLP  
 YP\* (SEQ ID NO: 110)

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

- response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response
- 5 can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.
- 10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.
- 15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.
- 20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class
- 25 of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to
- 30 function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).
- 35 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5   Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898. )

## Further references

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## Claims

1. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying  
5 expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein or encoding a protein comprising a ligand for said complex.
- 10 2. A method according to claim 1 allowing modulating cellular division during plant growth or organ formation
3. A method according to claim 2 wherein said gene comprises  
15 an RKS4 or RKS10 gene or functional equivalent thereof.
4. A method according to claim 1 allowing modulating apical meristem formation.
- 20 5. A method according to claim 4 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof.
6. A method according to claim 4 allowing modulating  
25 fasciation.
7. A method according to claim 6 wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent  
30 thereof.
8. A method according to claim 4 allowing modulating root development.
9. A method according to claim 7 wherein said gene comprises  
35 an ELS1, ELS 2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.



10. A method according to claim 4 allowing modulating meristem identity.
11. A method according to claim 9 wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof.
12. A method according to claim 1 allowing modulating pollen development.
- 10 13. A method according to claim 11 wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.
- 15 14. A method for providing resistance to a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising NDR/NHL protein, or encoding a protein comprising a ligand for said complex.
- 20 15. A method for obtaining a plant or plant cell with a modulated development comprising subjecting a plant or plant cell to a method according to anyone of claims 1 to 13.
- 25 16. A method for obtaining a resistant plant or plant cell comprising subjecting a plant or plant cell to a method according to claim 14.
- 30 17. A plant or plant cell obtainable with a method according to claim 15 or 16.

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(71) Applicant (for all designated States except US): EX-  
PRESSIVE RESEARCH B.V. [NL/NL]; Bornsesteeg 59,  
NL-6708 PD Wageningen (NL).

(72) Inventor; and

(75) Inventor/Applicant (for US only): SCHMIDT, Eduard,  
Daniel, Leendert [NL/NL]; Boelaertslaan 41, NL-6861 AT  
Oosterbeek (NL).

(74) Agent: PRINS, A.W.; Nieuwe Parklaan 97, NL-2587 BN  
Den Haag (NL).

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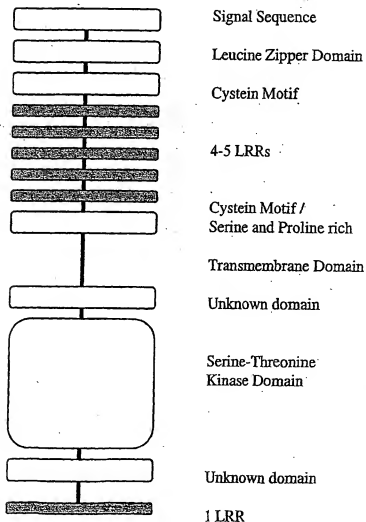
(54) Title: MODULATING DEVELOPMENTAL PATHWAYS IN PLANTS

(57) Abstract: The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein.

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Fig. 1

Different domains of RKS proteins



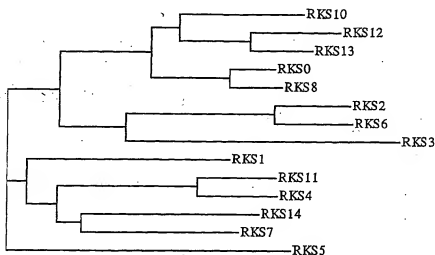
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Fig. 2

Developmental tree of the different Receptor Kinases like SERK (RKS) genes.



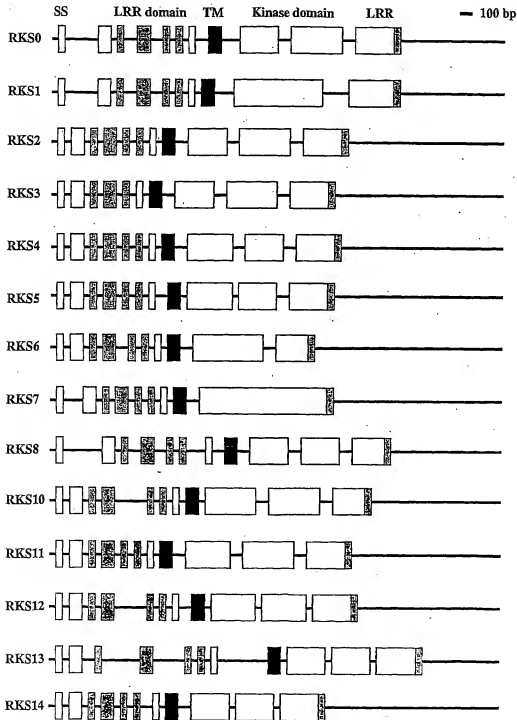
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Fig. 3

Intron-Exon structure of the RKS genes in *Arabidopsis thaliana* var. Columbia.  
 SS signal sequence; LRR leucine rich repeat domain; TM transmembrane domain.



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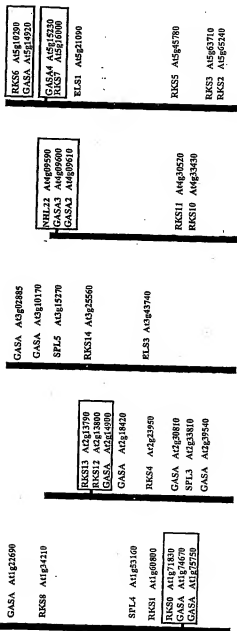
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Fig. 4

Chromosomal location of RKS genes  
 in *Arabidopsis thaliana*

I II III IV V



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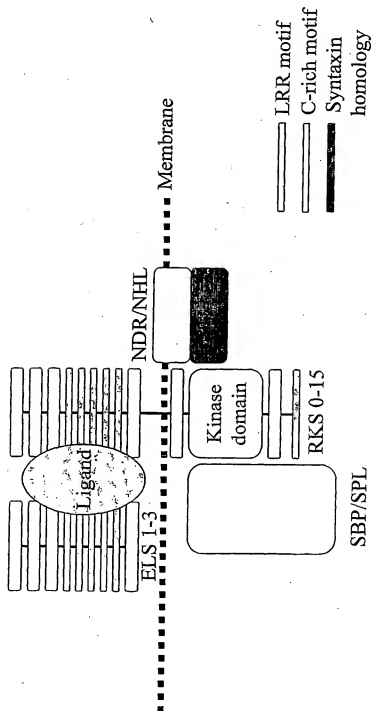
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Fig. 5

RKS-mediated signal transduction  
 pathway in plants



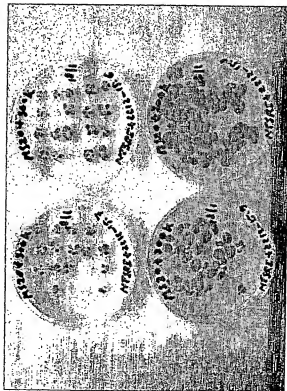
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GT-RKS4 determines seedling size  
in *Nicotiana tabacum*.



Modifications in the  
expression profile  
of GT-RKS4 modulates  
organ size within seedlings  
of *Nicotiana tabacum*.



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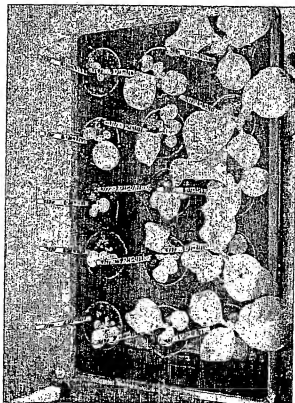
Fig. 7

GT-RKS4-7S-T2

GT-RKS4-6S-T2

GT-RKS4-3S-T2

GT-RKS4 determines organ size  
in *Nicotiana tabacum*.



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Fig. 8

GT-RKS4 determines plant size  
 in *Nicotiana tabacum*



GT-RKS4-15S-7T2



GT-RKS4-15S-6T2



Empty vector control



GT-RKS4-15S-9T2



GT-RKS4-15S-3T2

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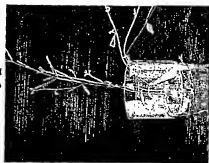
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Fig. 9

Stable transformed GT-RKS4-antisense  
in *Arabidopsis thaliana*

Wildtype WS



GT-RKS4-16a



Overexpression of antisense GT-RKS4-1a  
reduces plant and organ size.

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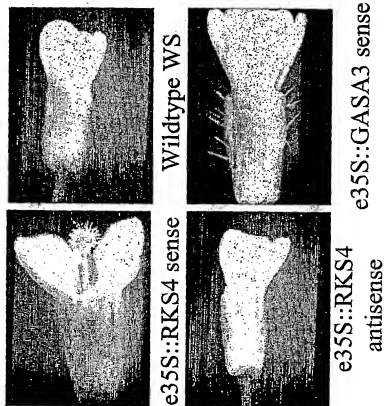
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Fig. 10

Ectopic expression of RKS4 and GAS3  
 gene products both result in increases  
 flower size in *Arabidopsis thaliana* WS

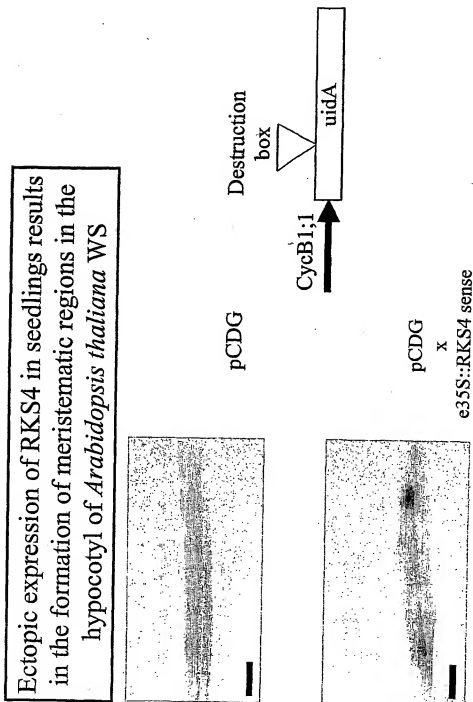


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Fig. 11



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Fig. 12

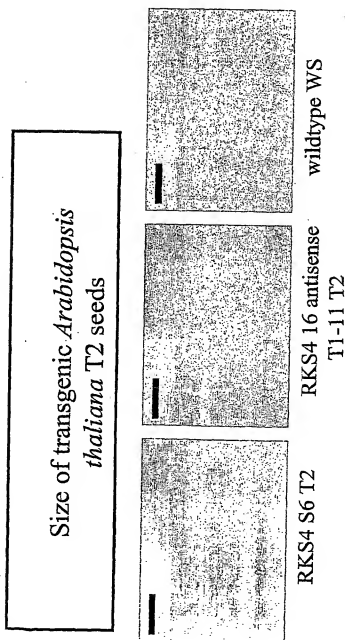


Fig. 13

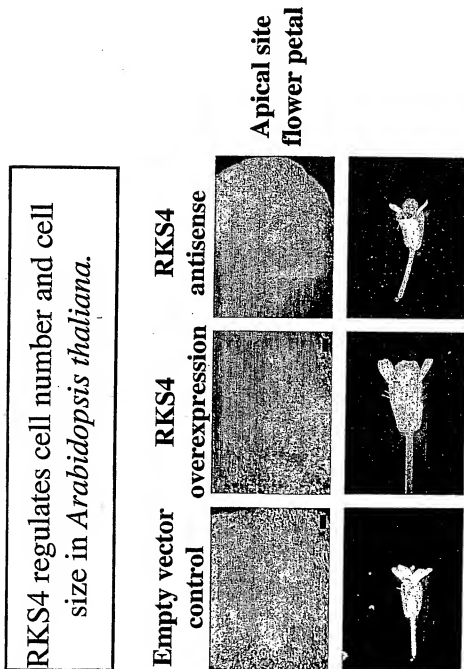
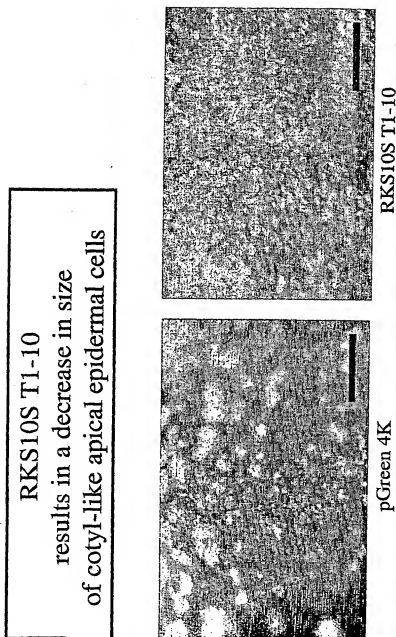


Fig. 14





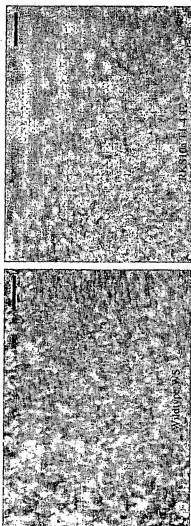
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Fig. 15

RKS10antisense T1-4  
results in an increase in size  
of the cotyl epidermal cells



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Fig. 16

Flower development from the same  
influorescence in transgenic  
*Arabidopsis thaliana*

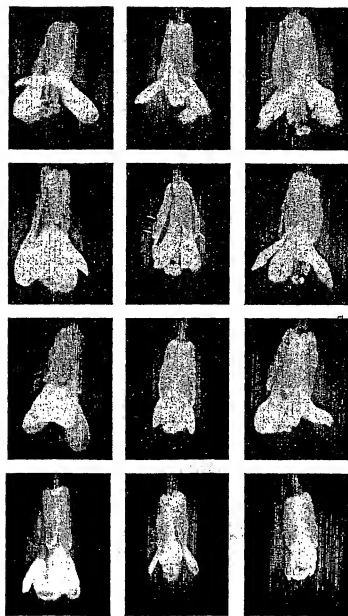
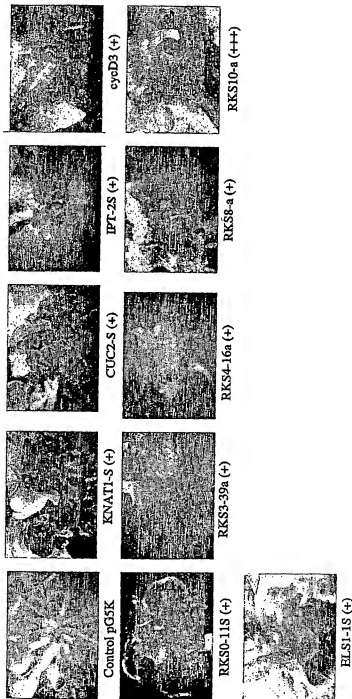


Fig. 17

Regeneration potential of  
*Arabidopsis* transgenic seedlings.



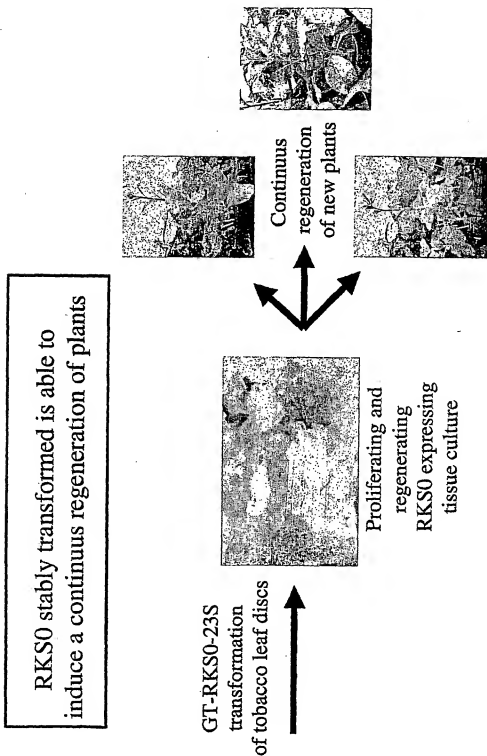
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Fig. 18



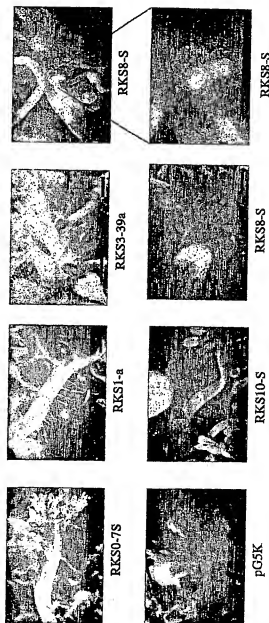
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Fig. 19

Fasciation in transgenic  
*Arabidopsis thaliana*



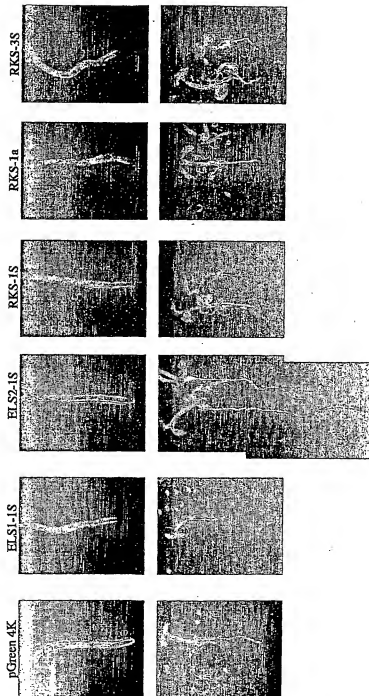
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Fig. 20

Root growth of transgenic  
*Arabidopsis thaliana*



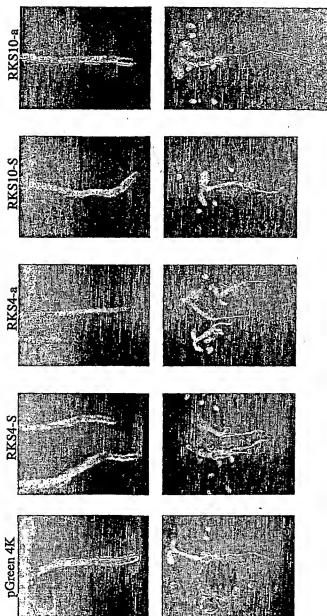
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Fig. 21

Root growth of transgenic  
*Arabidopsis thaliana*



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Fig. 22

Root growth of transgenic  
*Arabidopsis thaliana*

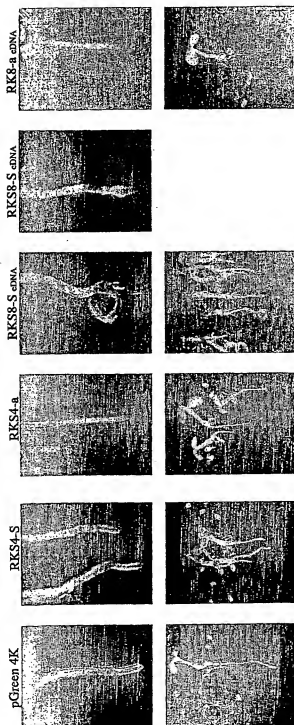
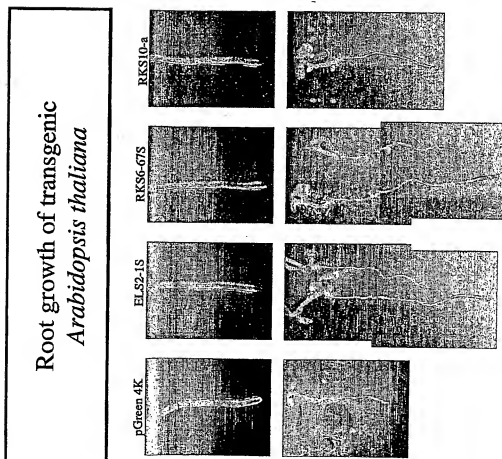


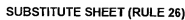


Fig. 23



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Fig. 24



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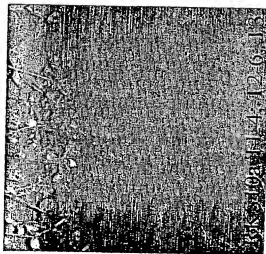
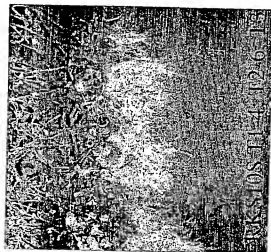
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Fig. 25

Effects of RKS10 transgenic  
constructs on plant development  
of 45 days old *Arabidopsis* WS



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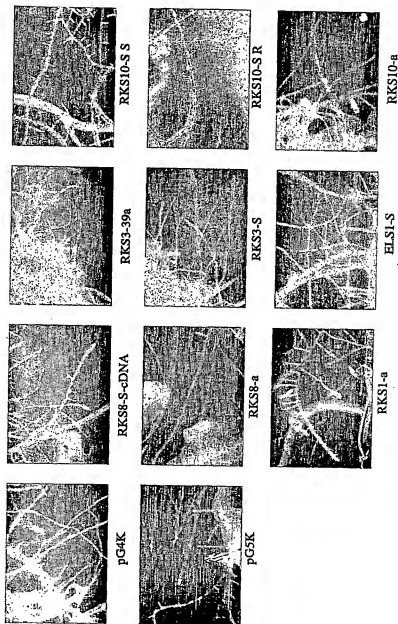
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Fig. 26

Roots of Transgenic  
*Arabidopsis thaliana*



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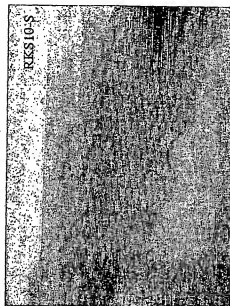
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Fig. 27

Root cells of transgenic  
*Arabidopsis thaliana*



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Fig. 28

Influorescences of T1 transgenic  
*Arabidopsis* WS plants

ELS-1-T1



RKS8-a-T1-10



RKS10-a-T2



RKS10-S-T1-10



Control pGreen4K



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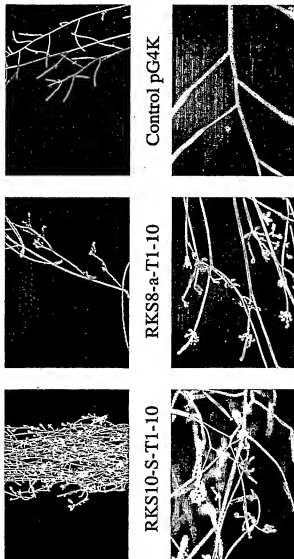
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Fig. 29

Influences of T1 transgenic  
*Arabidopsis* WS plants







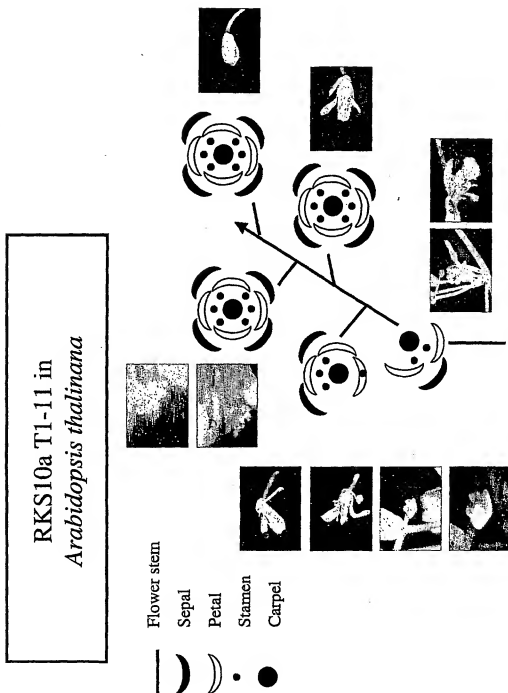
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Fig. 31



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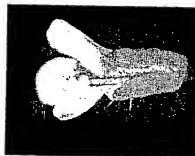
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Fig. 32

RKS10 antisense effects in  
*Arabidopsis thaliana*



pGreen 4K



RKS10a T1-11



detail flower RKS10a T1-11



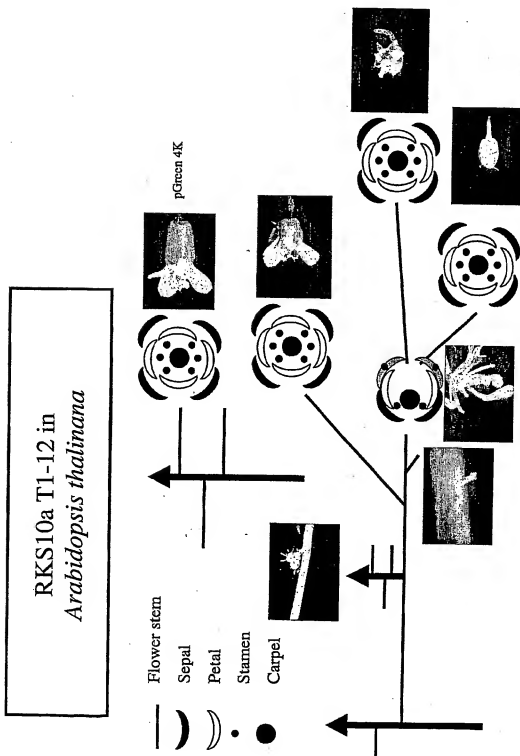
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Fig. 33



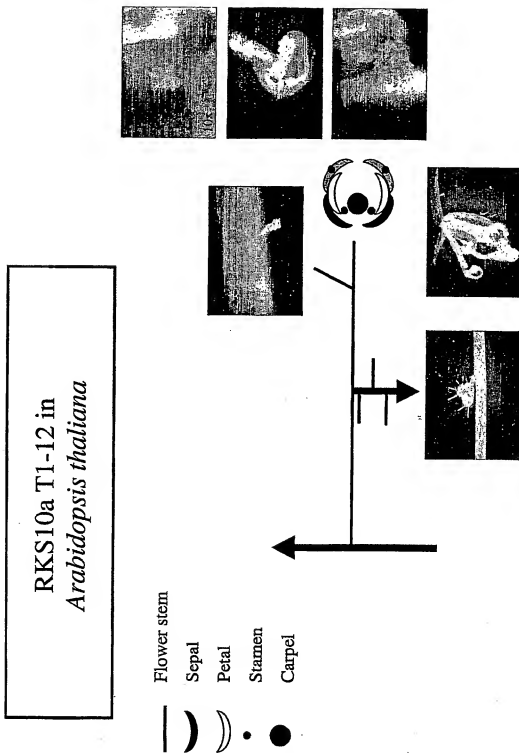
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Fig. 34



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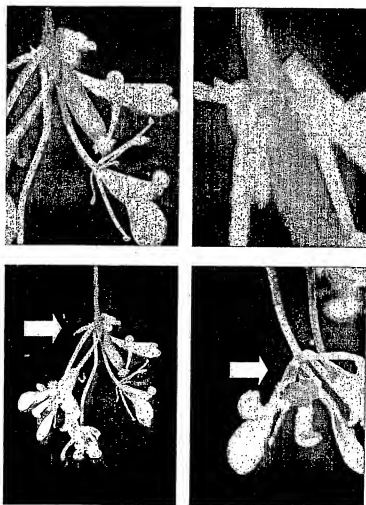
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Fig. 35

RKS13 regulates  
flower meristem identity in  
*Arabidopsis thaliana*



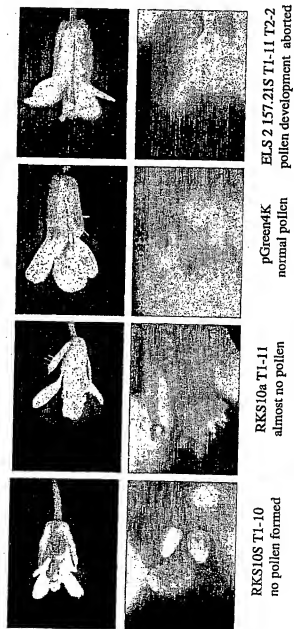
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Fig. 36

Male sterile transgenes in  
*Arabidopsis thaliana*



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